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(54) Title: GENES FOR ALTERING MITOCHONDRIAL FUNCTION AND FOR HYBRID SEED PRODUCTION

(57) Abstract: The present invention relates to isolated nucleic acid molecules which restore fertility to cytoplasmic male sterile plants and modify expression of toxic mitochondria proteins by the plant. The present invention also relates to methods of identifying a candidate plant suitable for breeding with a cytoplasmic male sterile plant and methods of identifying a candidate gene restoring fertility in plants by analyzing for the candidate plant and candidate gene, respectively, for the presence of the nucleic acid molecule of the present invention. Also disclosed are methods of producing hybrid plant seed, methods of directing gene expression to plant mitochondria, and method of expressing a gene preferentially in roots of a plant. Promoters and terminators from plant genes which restore fertility to cytoplasmic male sterile plants and modify expression of toxic mitochondria proteins are also disclosed. Finally, methods of producing plants with a cytoplasmic male sterile plant restoration system are disclosed.

GENES FOR ALTERING MITOCHONDRIAL FUNCTION AND FOR HYBRID SEED PRODUCTION

[0001] This application claims the benefit of U.S. Patent Application Serial No. 60/347,996, filed January 10, 2002, which is hereby incorporated by reference in its entirety.

[0002] This invention arose out of research sponsored by the USDA NRI (Grant No. 98-35300-6171). The U.S. Government may have certain rights in this invention.

FIELD OF THE INVENTION

[0003] The present invention relates to improving productivity or usefulness of plants by altering mitochondrial gene expression and to the production of hybrid seed. Specifically, the present invention relates to the use of genes that affect mitochondrial gene expression, some of which ameliorate male sterility and others which cause male sterility or altered floral development. The invention also provides a method of facilitating the identification of genes with similar functions in other plant species.

BACKGROUND OF THE INVENTION

[0004] A widely used method for producing hybrid seeds involves crossing a cytoplasmic male sterile (CMS) plant line with a fertile plant line. Typically, the fertile line contains a fertility restorer gene in its nuclear genome, so that all of the progeny are male fertile. All seeds collected from a CMS plant must result from cross-pollination. However, the hybrid seed so generated will itself be male sterile unless the male parent has brought a nuclear fertility-restorer gene into the next generation. The fertility of the progeny is important for productivity in plant varieties where self-pollination is responsible for production of the desirable crop. For example, a fruit crop of a self-pollinated species requires male fertility, while an ornamental species will produce attractive flowers or plant morphology even when no pollen is produced.

[0005] While a number of naturally occurring CMS/restorer systems exist and are currently in use for hybrid seed production, there are a number of crop species which lack known CMS and fertility restorer genes. For example, a hybrid seed of tomato is typically made by hand emasculation of plants to be used as female parents. This hand-made method of cross-pollination is quite labor intensive and cost-prohibitive for many crops. In addition, certain naturally occurring CMS/restorer systems have some drawbacks. For example, corn plants carrying the CMS-T cytoplasm are more susceptible to a blight disease.

[0006] Fertility restorer genes that have been particularly useful for hybrid seed production are active as single dominant alleles at a locus, though multigenic systems are sometimes used. A *Petunia* fertility restorer locus termed *Rf* is known to be effective with no additional helper genes to restore fertility (Edwardson et al., "Fertility Restoration in Cytoplasmic Male Sterile *Petunia*," J. Hered., 58:195-196 (1967); Izhar, "Cytoplasmic Male Sterility in Petunia. III. Genetic Control on Microsporogenesis and Male Fertility Restoration," J. Hered., 69:22-26 (1978)).

[0007] Nuclear fertility restoration genes confer normal pollen development upon plants carrying sterility-encoding mitochondria. The mitochondrial genes responsible for causing the male sterility have been identified in a number of species, including *Petunia*, maize, *Brassica*, and common bean. The expression of these CMS-encoding mitochondrial genes is affected by the nuclear restorer genes, as shown for *Rf* in *Petunia* (Pruitt et al., "Cytochrome Oxidase Subunit II Sequences in *Petunia* Mitochondria: Two Intron-Containing Genes and an Intron-Less Pseudogene Associated With Cytoplasmic Male Sterility," Curr. Genet., 16:281-91 (1989); Nivison et al., "Identification of a Mitochondrial Protein Associated With Cytoplasmic Male Sterility in *Petunia*," Plant Cell, 1:1121-30 (1989); Nivision et al., "Sequencing, Processing, and Localization of the *Petunia* CMS-Associated Mitochondrial Protein," Plant J., 5:613-623 (1994); Hanson et al., "Mitochondrial Gene Organization and Expression in Petunia Male Fertile and Sterile Plants," J. Hered., 90:362-368 (1999)); *Rf1* in CMS-T maize (Dewey et al., "Novel Recombinations in the Maize Mitochondrial Genome Produce a Unique Transcriptional Unit in the Texas Male-Sterile Cytoplasm," Cell, 44:439-49 (1986); Wise et al., "Mitochondrial Transcript Processing and Restoration of Male Fertility in T-Cytoplasm Maize," J Hered, 90:380-385 (1999); Kennell et al., "Influence of

Nuclear Background on Transcription of a Maize Mitochondrial Region Associated With Texas Male Sterile Cytoplasm," Mol. Gen. Genet., 210:399-406 (1987); Kennell et al., "Initiation and Processing of *atp6*, T-*urf13*, and *ORF221* Transcripts From Mitochondria of T Cytoplasm Maize," Mol. Gen. Genet., 216:16-24 (1989)); *Rfp1* and *rfp1* in *Brassica* (Singh et al., Suppression of Cytoplasmic Male Sterility by Nuclear Genes Alters Expression of a Novel Mitochondrial Gene Region," Plant Cell, 3:1349-1362 (1991); Singh et al., "Nuclear Genes Associated With a Single Brassica CMS Restorer Locus Influence Transcripts of Three Different Mitochondrial Gene Regions," Genetics, 143:505-516 (1996)); restorers in radish (Krishnasamy et al., "Organ-Specific Reduction in the Abundance of a Mitochondrial Protein Accompanies Fertility Restoration in Cytoplasmic Male-Sterile Radish," Plant Molec. Biol., 26:935-946 (1994)); restorers in sunflower (Horn et al., "A Mitochondrial 16 kDa Protein is Associated With Cytoplasmic Male Sterility in Sunflower," Plant Molec. Biol., 17:29-36 (1991); Laver et al., "Mitochondrial Genome Organization and Expression Associated With Cytoplasmic Male Sterility in Sunflower (*Helianthus annuus*)," Plant J., 1:185-193 (1991); Monéger et al., "Nuclear Restoration of Cytoplasmic Male Sterility in Sunflower is Associated With the Tissue-Specific Regulation of a Novel Mitochondrial Gene," EMBO J., 13:8-17 (1994); Smart et al., "Cell-Specific Regulation of Gene Expression in Mitochondria During Anther Development in Sunflower," Plant Cell, 6:811-825 (1994)); restorers in rice (Akagi et al., "A Unique Sequence Located Downstream From the Rice Mitochondrial *atp6* May Cause Male Sterility," Curr. Genet., 25:52-58 (1994); Kadowaki et al., "A Chimeric Gene Containing the 5' Portion of *atp6* is Associated With Cytoplasmic Male Sterility of Rice," Mol. Gen. Genet., 224:10-16 (1990)); and *Fr2* in broad bean (Chase, "Expression of CMS-Unique and Flanking Mitochondrial DNA Sequences in *Phaseolus vulgaris*," L. Curr. Genet., 25:245-251 (1993); He et al., "Pollen Fertility Restoration by Nuclear Gene *Fr* in CMS Bean: Nuclear-Directed Alteration of a Mitochondrial Population," Genetics, 139:995-962 (1995)). The expression of various nuclear restorer genes has been reported to be either enhanced in reproductive tissue, as in the case of sunflower, or, as in the case of *Petunia*, expressed in both vegetative and reproductive tissues. Thus, different fertility restorer genes carry different promoters and nuclear expression regulatory elements which may confer very limited tissue-specific expression or very broad expression in the plant.

[0008] Reduction in the amount of the protein product of the CMS-encoding gene is the usual effect of these restorers whose target mitochondrial genes are known. These genes may possibly act by affecting the transcription or translation rate, the transcript or protein stability, processing, splicing, etc. Alleles of some restorer genes may up-regulate while others may down-regulate the expression of particular mitochondrial genes. Fertility restorer genes and their alleles or homologous counterparts in other species may thus be extremely valuable in engineering the expression of genes introduced into higher plant mitochondria.

[0009] The cloning and sequencing of the restorer gene *Rf2* in maize has been reported in Cui et al., "The *rf2* Nuclear Restorer Gene of Male-Sterile T-Cytoplasm Maize," Science, 272:1334-1336 (1996) and U.S. Patent No. 5,981,833 to Wise et al. This restorer gene acts in conjunction with a second required gene, *Rf1*, the gene that reduces the amount of the toxic protein, to restore fertility to plants carrying the maize CMS-T cytoplasm (Dewey et al., "Novel Recombinations in the Maize Mitochondrial Genome Produce a Unique Transcriptional Unit in the Texas Male-Sterile Cytoplasm," Cell, 44:439-49 (1986); Dewey et al., "A Mitochondrial Pprotein Associated With Cytoplasmic Male Sterility in the T Cytoplasm of Maize," Proc. Natl. Acad. Sci. USA, 84:5374-78 (1987); Wise et al., "*Urf13-T* of T Cytoplasm Maize Mitochondria Encodes a 13kD Polypeptide," Plant Mol. Biol., 9:121-26 (1987)). Plants of genotype *Rf1rf2*, though sterile, have greatly reduced amounts of the URF13 protein. In contrast, sterile plants of genotype *rf1Rf2* have abundant amounts of the URF13 protein. The *Rf2* gene is, thus, unusual in that no effect on the expression of the maize T-CMS-associated protein, URF13, has been detected. The sequence of the gene bore out the absence of observable effect on mitochondrial gene expression; according to sequence analysis, *Rf2* is apparently an aldehyde dehydrogenase (Liu et al., "Mitochondrial Aldehyde Dehydrogenase Activity is Required for Male Fertility in Maize," The Plant Cell, 13:1063-1078 (2001)). It has been proposed that *Rf2* acts by compensating for a metabolic defect caused by the low levels of the URF13 protein that remain despite the presence of *Rf1*, the gene that reduces the amount of the toxic protein (Dewey et al., "A Mitochondrial Protein Associated With Cytoplasmic Male Sterility in the T Cytoplasm of Maize," Proc. Natl. Acad. Sci. USA, 84:5374-78 (1987)) and also alters the T-*urf13* transcript profile (Kennell et al., "Influence of Nuclear Background on Transcription of a Maize

Mitochondrial Region Associated With Texas Male Sterile Cytoplasm," Mol. Gen. Genet., 210:399-406 (1987)).

[0010] An abnormal recombinant mitochondrial gene in *Petunia* CMS lines (termed *pcf*) has been genetically correlated with CMS (Young et al., "A Fused Mitochondrial Gene Associated With Cytoplasmic Male Sterility is Developmentally Regulated," Cell, 50:41-49 (1987)). Because plant mitochondrial RNA is edited from C to U in some locations, the edited RNA sequence for the *pcf* gene has been determined, allowing the prediction of the *pcf*-encoded protein (Wintz et al., "A Termination Codon is Created by RNA Editing in the *Petunia* Mitochondrial *atp9* Gene Transcript," Curr. Genet., 19:61-64 (1990); Sutton et al., "Editing of Pre-mRNAs Can Occur Before *cis*- and *trans*-Splicing in *Petunia* Mitochondria," Mol. Cell Biol., 11:4274-4277 (1991); Nivision et al., "Sequencing, Processing, and Localization of the *Petunia* CMS-Associated Mitochondrial Protein," Plant J., 5:613-623 (1994); Hanson et al., "Mitochondrial Gene Organization and Expression in Petunia Male Fertile and Sterile Plants," J. Hered., 90:362-368 (1999)). Antibodies to synthetic peptide sequences have revealed the presence of a 19.5 kD PCF protein located in both the membrane and soluble fraction of mitochondria (Nivison et al., "Identification of a Mitochondrial Protein Associated With Cytoplasmic Male Sterility in *Petunia*," Plant Cell, 1:1121-30 (1989)). The PCF protein is processed from a longer precursor protein and is entirely encoded by the *urfS* region of the *pcf* gene (Nivision et al., "Sequencing, Processing, and Localization of the *Petunia* CMS-Associated Mitochondrial Protein," Plant J., 5:613-623 (1994)). The PCF protein is strongly expressed in sporogenous cells of premeiotic petunia anthers in CMS lines, but undetectable in CMS-*Rf* lines (Conley et al., "Tissue-Specific Protein Expression in Plant Mitochondria," Plant Cell, 6:85-91 (1994)). Abnormalities in *Petunia* pollen development are first observed in meiosis, and by the developmental stage where fertile plants are releasing pollen, CMS anthers are hollow shells (Conley et al., "Effects of *Petunia* Cytoplasmic Male Sterile (CMS) Cytoplasm on the Development of Sterile and Fertility-Restored *P. parodii* Anthers," Am. J. Bot., 81:630-640 (1994)). It is evident that the *pcf* gene product is disrupting mitochondrial function, leading to death of the sporogenous cells, though the exact mechanism at the molecular level is not known.

[0011] In maize T, *Petunia*, rice, and *Brassica* Pol CMS systems, particular transcripts of CMS-associated genes have been reported to be altered in restored lines (Pruitt et al., "Transcription of the *Petunia* Mitochondrial CMS-Associated *pcf* Locus in Male Sterile and Fertility-Restored Lines," Mol. Gen. Genet., 227:348-355 (1991); Dewey et al., "Novel Recombinations in the Maize Mitochondrial Genome Produce a Unique Transcriptional Unit in the Texas Male-Sterile Cytoplasm," Cell, 44:439-49 (1986); Kennell et al., "Initiation and Processing of *atp6*, T-*urf13*, and *ORF221* Transcripts From Mitochondria of T Cytoplasm Maize," Mol. Gen. Genet., 216:16-24 (1989); Kennell et al., "Influence of Nuclear Background on Transcription of a Maize Mitochondrial Region Associated With Texas Male Sterile Cytoplasm," Mol. Gen. Genet., 210:399-406 (1987); Singh et al., "Suppression of Cytoplasmic Male Sterility by Nuclear Genes Alters Expression of a Novel Mitochondrial Gene Region," Plant Cell, 3:1349-1362 (1991); Singh et al., "Nuclear Genes Associated With a Single Brassica CMS Restorer Locus Influence Transcripts of Three Different Mitochondrial Gene Regions," Genetics, 143:505-516 (1996); Wise et al., "Mitochondrial Transcript Processing and Restoration of Male Fertility in T-Cytoplasm Maize," J. Hered., 90:380-385 (1999)). In *Brassica*, the presence of either one of two restorer genes results in monocistronic transcripts of *atp6*, instead of the dicistronic *orf224/atp6* transcripts found in CMS lines (Singh et al., "Suppression of Cytoplasmic Male Sterility by Nuclear Genes Alters Expression of a Novel Mitochondrial Gene Region," Plant Cell, 3:1349-1362 (1991)). A UG-rich sequence appears to be the target of the *Brassica* restorer alleles (Singh et al., "Nuclear Genes Associated With a Single *Brassica* CMS Restorer Locus Influence Transcripts of Three Different Mitochondrial Gene Regions," Genetics, 143:505-516 (1996)). In *Petunia*, *pcf* transcripts with 5' termini at -121 are specifically reduced in restored lines (Pruitt et al., "Transcription of the *Petunia* Mitochondrial CMS-Associated *pcf* Locus in Male Sterile and Fertility-Restored Lines," Mol. Gen. Genet., 227:348-355 (1991)), while transcripts terminating at -266 and -522 remain at normal levels. In maize T cytoplasm, a sequence unlike either the *Brassica* restorer target or the *Petunia* -121 transcript terminus is the putative recognition signal for the *Rf1* gene (Dill et al., "*Rf8* and *Rf** Mediate Unique T-urf13-Transcript Accumulation, Revealing a Conserved Motif Associated With RNA Processing and Restoration of Pollen Fertility in T-cytoplasm Maize," Genetics, 147:1367-1379 (1997)).

[0012] The steady-state amounts of the *Petunia pcf*-encoded protein and the maize *urf13*-encoded protein decrease greatly in restored lines compared to unrestored lines (Nivison et al., "Identification of a Mitochondrial Protein Associated With Cytoplasmic Male Sterility in *Petunia*," Plant Cell, 1:1121-30 (1989); Dewey et al., "Novel Recombinations in the Maize Mitochondrial Genome Produce a Unique Transcriptional Unit in the Texas Male-Sterile Cytoplasm," Cell, 44:439-49 (1986); Wise et al., "*Urf13-T* of T Cytoplasm Maize Mitochondria Encodes a 13kD Polypeptide," Plant Mol. Biol., 9:121-26 (1987)). Abundance of CMS-associated proteins is also reduced in sunflower and radish (Horn et al., "A Mitochondrial 16 kDa Protein is Associated With Cytoplasmic Male Sterility in Sunflower," Plant Mol. Biol., 17:29-36 (1991); Laver et al., "Mitochondrial Genome Organization and Expression Associated With Cytoplasmic Male Sterility in Sunflower (*Helianthus annuus*)," Plant J., 1:185-193 (1991); Krishnasamy et al., "Organ-Specific Reduction in the Abundance of a Mitochondrial Protein Accompanies Fertility Restoration in Cytoplasmic Male-Sterile Radish," Plant Mol. Biol., 26:935-946 (1994)). The mechanism behind the reduction in quantity of CMS-associated proteins in restored lines is not understood. For example, absence of transcripts that could potentially encode the PCF protein is not the explanation; only the shortest transcript is reduced in restored lines (Pruitt et al., "Transcription of the *Petunia* Mitochondrial CMS-Associated *pcf* Locus in Male Sterile and Fertility-Restored Lines," Mol. Gen. Genet., 227:348-355 (1991)).

[0013] In *Petunia* and in some other CMS/restorer systems, the abnormal gene is co-transcribed with known mitochondrial genes. One possible mechanism for CMS in *Petunia* and its restoration, which is also consistent with current data, is that the restorer gene not only results in decrease in the expression of PCF, but also improves the expression of the co-transcribed genes *nad3* and *rps12* in some way. For example, it remains possible that an RNA processing event results in little translation of PCF but enhanced production of NAD3 and RPS12 protein.

[0014] In sum, with the exception of maize *Rf2*, in those systems where analysis has reached the molecular level, restorer genes have been found to affect the abundance of mitochondrial-encoded DNAs, RNAs, and proteins.

[0015] Cytoplasmic male sterility/restorer systems have been proven to be an invaluable tool in the production of hybrid seeds. Despite their importance for both

the production of major crops such as rice and sunflower and the study of organelle/nuclear interactions in plants, none of the nuclear fertility-restorer genes that reduce the expression of aberrant mitochondrial proteins have been cloned.

[0016] The present invention is directed to overcoming these deficiencies in the art.

SUMMARY OF THE INVENTION

[0017] The present invention relates to an isolated nucleic acid molecule which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant. The nucleic acid molecule encodes a protein having an amino acid sequence of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, or 41. Alternatively, the nucleic acid molecule encodes a protein containing a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input. Alternatively, the nucleic acid molecule hybridizes to a nucleotide sequence of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, or SEQ ID NO: 40 under stringent conditions of a hybridization buffer containing 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C. Alternatively, the nucleic acid molecule has a nucleotide sequence of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, or SEQ ID NO: 40.

[0018] Another aspect of the present invention relates to a method of identifying a candidate plant suitable for breeding with a cytoplasmic male sterile plant. The method involves analyzing the candidate plant for the presence, in its genome, of the above nucleic acid molecule of the present invention.

[0019] Yet another aspect of the present invention relates to a method of identifying a candidate gene restoring fertility in plants. The method involves analyzing the candidate gene for the presence of the above nucleic acid molecule in accordance with the present invention.

[0020] The present invention also relates to a method of producing hybrid plant seed. The method first involves providing a cytoplasmic male sterile plant. Next, a second plant containing the above nucleic acid molecule in accordance with the present invention is provided. Finally, the cytoplasmic male sterile plant and the second plant are bred under conditions effective to produce hybrid progeny seed which yield fertile plants.

[0021] Another aspect of the present invention relates to a method of producing plant seeds for an inbred line of plants. The method first involves providing a cytoplasmic male sterile plant. Next, a second plant containing the above nucleic acid molecule in accordance with the present invention is provided. Then, the cytoplasmic male sterile plant and the second plant are bred under conditions effective to produce hybrid progeny seed which yield fertile plants. Next, hybrid fertile plants are produced from the hybrid progeny seeds. Finally, the hybrid fertile plants and the second plant are backcrossed to produce seed which yiled inbred progeny plants.

[0022] Yet another aspect of the present invention relates to a method of directing gene expression to plant mitochondria. The method involves transforming a plant with a chimeric nucleic acid molecule containing a transgene operatively linked to a promoter or a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant. The promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1. The terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

[0023] The present invention also relates to a promoter from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant. The promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1.

[0024] Another aspect of the present invention relates to a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant. The terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

[0025] Yet another aspect of the present invention relates to a nucleic acid construct. The nucleic acid construct includes: (i) a promoter or a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant and (ii) a nucleic acid heterologous to and operatively coupled to the promoter or the terminator. The promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1. The terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

[0026] The present invention also relates to a method of expressing a gene preferentially in roots of a plant. The method involves transforming a plant with a nucleic acid construct. The nucleic acid construct includes a promoter suitable for driving expression preferentially in roots having a nucleotide sequence of from 1 to 1388 of SEQ ID NO: 44; a nucleic acid heterologous to the promoter, where the promoter is operatively coupled 5' to the nucleic acid to induce transcription of the nucleic acid; and a terminator having a nucleotide sequence of from nucleotide 3168 to 4016 of SEQ ID NO: 44, where the terminator is operably coupled 3' to the nucleic acid.

[0027] Another aspect of the present invention relates to a method of altering plant floral morphology in ornamental plants. The method involves transforming an ornamental plant with the above nucleic acid molecule in accordance with the present invention.

[0028] Another aspect of the present invention relates to a method of producing plants with a cytoplasmic male sterile plant restoration system. The method first involves transforming a first plant in its chloroplast genome with a nucleic acid which causes the plant to become male sterile. Next a second plant is transformed with the above nucleic acid molecule in accordance with the present

invention whose protein product is targeted to the chloroplast. Finally, the first and second plants are crossed to produce progeny plants possessing a cytoplasmic male sterile plant restoration system.

[0029] Another aspect of the present invention relates to a method of producing plants with a cytoplasmic male sterile plant restoration system. The method first involves mutagenizing a first plant having a nucleic acid which encodes a protein. The protein has a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input. Next, the mutagenized first plant is crossed with a wild-type plant having mitochondrial DNA polymorphisms compared to mitochondrial DNA in the mutagenized first plant to produce progeny plants. Finally, it is determined if the progeny plants are fertile, whereby fertile progeny plants can be used as a fertile maintainer line, where the mutagenized first plant, the fertile maintainer line, and a wild-type allele present in the first plant before mutagenesis comprises a new cytoplasmic male sterile plant restoration system.

[0030] The present invention also relates to an isolated nucleic acid sequence corresponding to SEQ ID NO: 42 or SEQ ID NO: 44.

[0031] The present invention identifies nucleic acid sequences which encode the gene for restoration of fertility to cytoplasmic male sterile plants. This gene modifies the expression of the mitochondrial genome and is the first such gene sequence that has been identified. In petunia, the gene may be transferred to lines lacking the gene in order to restore fertility. More importantly, the gene sequence has characteristics that can be used to identify comparable genes from economically important species. Thus, the gene and the sequence information may be used to develop hybrid seed production systems in economically important plants. Furthermore, the information may be used in crop improvement by controlling mitochondrial gene expression.

BRIEF DESCRIPTION OF THE DRAWINGS

[0032] Figures 1A-D show that the *Rf* locus contains two tandem mitochondrially targeted PPR motif genes. Figure 1A illustrates the genomic organization of the region containing the *Rf-PPR592* and *Rf-PPR591* genes. Duplicated blocks are indicated by similar shading. Arrows indicate the direction of transcription. 1 and 2 show locations of the primers used to amplify the *rf-PPR592* gene from a CMS plant. Figure 1B shows a single onion epidermal cell expressing a known mitochondrially targeted green fluorescent protein (GFP) after DNA bombardment. Figure 1C shows a single onion epidermal cell transiently expressing 44 N-terminal amino acids of Rf-PPR592 fused to GFP. Figure 1D shows a comparison of PPR motifs found in Rf-PPR592 with the MEME-derived consensus from 1,303 PPR motifs. The 14 PPR repeats are sorted by decreasing statistical significance, with PPR 230-264 showing the highest match to the consensus motif that is generated by retaining only the amino acids that occur at least in 6 of the 14 repeats.

[0033] Figures 2A-B show the genetic structure of the *rf-PPR592* gene. Figure 2A illustrates that a comparison of *Rf-PPR592* and *rf-PPR592* reveals a size polymorphism. The first lane was loaded with the *Rf-PPR592* PCR amplicon obtained from a restorer line (*Rf/Rf*), the adjacent lane was loaded with the *rf-PPR592* PCR amplicon obtained with the same primer pair from a CMS line (*rf/rf*). Figure 2B illustrates that a comparison of *Rf-PPR592, Rf-PPR591,* and *rf-PPR592* reveals five similarity blocks. For each block, (I to V), the two blocks that exhibit the greatest similarity are shown with the same shading. Overall all three sequences are greater than 90% identical at the nucleotide level except in block V, where *Rf-PPR591* exhibits only 23% identity to the other two genes. The locations of 47- and 49-nt deletions in *Rf-PPR591* and 47- and 530-nt deletions in *rf-PPR592* with respect to the *Rf-PPR592* sequence in blocks I and II are shown as lines.

[0034] Figures 3A-B show the expression pattern of *rf-PPR592* and *Rf-PPR592*. Figure 3A depicts the examination of floral bud RNA for expression of *rf-PPR592* and *Rf-PPR592*. RT-PCR of floral bud RNA of a CMS plant (S) with primers specific to *rf-PPR592*, and RT-PCR of floral bud RNA of an *Rf/Rf* (nontransgenic) fertile plant with primers specific for *Rf-PPR592* (R). DNA, positive

control for the amplification where the substrate is leaf DNA from a CMS plant; M, mass markers; 0, no template added, negative control. Figure 3B depicts the examination of different tissues for expression of *rf-PPR592*. RT-PCR of RNA from different tissues of a CMS plant with primers specific to *rf-PPR592*. DNA, M, and 0 are same as in Figure 3A.

[0035] Figures 4A-D illustrate the restoration of fertility to CMS *Petunia* lines by transformation with a 4.6-kb genomic sequence carrying *Rf-PPR592*. Figure 4A shows the flower of *P. parodii* CMS line 3688. Figure 4B shows the regenerant carrying *Rf-PPR592*. Figure 4C shows the *P. hybrida* CMS line 2423. Figure 4D shows the regenerant carrying *Rf-PPR592*.

[0036] Figures 5A-B illustrate the cosegregation of the *Rf-PPR592* transgene, restoration of fertility, and reduction of PCF. Figure 5A shows the DNA blot hybridized with an *npt* II transgene-specific probe. Lane 1, *P. parodii* CMS line 3688; lanes 2-and 3, sterile T_1 progeny of transformed *P. parodii*; lanes 4-9, fertile T_1 progeny. Figure 5B shows the immunoblot of floral bud proteins probed with anti-PCF antibody. Lanes are as in Figure 5A.

[0037] Figures 6A-B illustrate abnormal flowers on plants obtained by introducing *Rf*-PPR592 into a CMS background. Figure 6A shows a petaloid flower on a plant carrying a recombination event near the *Rf* locus, affecting the region 5' to *Rf*-PPR592. Figure 6B shows an abnormal flower on a plant carrying the CMS cytoplasm and the 4.5 kb *Rf*-PPR592 transgene.

[0038] Figures 7A-B show methods for creating a new CMS/restorer system.

[0039] Figure 8 shows a two-line method for hybrid rice production, using an engineered inducible restorer gene.

DETAILED DESCRIPTION OF THE INVENTION

[0040] The present invention relates to an isolated nucleic acid molecule which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant.

[0041] One form of the nucleic acid molecule of the present invention is a nucleotide sequence of from nucleotide 1982 to 3760 of SEQ ID NO: 1, identified herein as *Rf-PPR592*, as follows:

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1    ATATATATATACAAACTGATTTTTTCTGTCTATTTGCACAGTGTTATATTTACATACCCTTGAAAAAGGGTAGCTCCGCT
81   AATAATGTTATCTTTACAAAAAATAACAATAATTTTTTTACATAATATATACAAAACTCATTGTTATGTATTGTAAATAT
161  GATAAAAATATTGTTATTTTTTGTAATATAGCTATTAGGTAGTCATGTGGTGTAATATTTCCTAAAAATATTTACCTGAG
241  TCGGCCATTTGGCTAAAAATATTTTATTTTATAGTCGCATATACTCCAAGCTTGTATATCCCATAGCGACAGTATACCTA
321  TACGATATCTTCTATTATTTACCTTTTTAGTATTCGTATACCCCCAATAGTATACAAGTTTGACACCGCAATAGTGTACC
401  CCAATGTTGTGGTTGTGTGGCTATAAAATGTTTAAACAAAATTTGAGTGATGGTAGTGTAATTTTTTAGTGTAAGCTGGG
481  TAGTTTTAAAAACATTCTTTTTGAAAATTGTAGTTCAAGTCATAGTACAAAAAACTGAAATATTTATATGTTTCTTGATT
561  TTGGCTGGTCTTCTAAAAATTTTGAAATGCTGGCTAGTTTTCATTTAGCGAGGGGCAAATAGACTACATGGCCAAATTTT
641  TACGTTAAAAGAAGTGTTGTCTGGGAAAGTATTCGAAAAGATTGTACGGACAAGTGTTGCCTAGACAACACGTCAAATTA
721  TGTAGAAAAATGTAGGAAGAAATTCAAAAGCAAATATTGCTTAAGCAAAAGGCAGTCAAAGACAATGCTGCCTTAGGGAG
801  TGAGAAATGGGCATCACTATAAGATTGTATTTCCATTCGATATTTATTCATTATAAACTTAAGGAAAAGTGCAAGGAAAA
881  GCCACTTTTTGGCTTGCCTTTACCGTTGAAGCTACTTTCAAAGAAAAAGAGCTAGTTTTTAGCTTTTTTGGAACTTTAAT
961  CATTGTGGGCCGAACTTCAGACCTTGTGGGCCGAACTTCATACATTCACAAGTAAAAAATTAGCTCACAGGCCACTTTTA
1041 CCACTAGTATTTGGTTTGAAGTCATTTTTTTTATTGGTTTTACATGAGAGACCACTTTTTGGAACTTCAATCTTTGTGCGC
1121 TTGAACTTCATGCCTAAGTTATTAAGTTCAACTTCAATCCGTAAGGGCTGAATTTTTAGGCATAGATGCGTAAACTTCAA
1201 CCTTGTGGACTGAAGTTGAACTTCGCCCCTTATGGTGGCCTGAAGTTGAACTTCAATCCTTGTGGGCTGAACTTGTGTGA
1281 AGTTCAACCCACAAGGATTAAAGTTTCAAAAAATGACCTCTCAAGCAAAATCTGCAAAAAAAAGTGGTCTCTCATGCACT
1361 TTTACCCATTCGCAAAGTAGGCTGAAGTTCAGCCCACAATTATTCAAGTTCCAAAAAATTTCACAATATATACCTCCTTA
1441 TCTCGGTTATGATCTTTTGTATGATTTAGCAAAATGGACGGGGAAAGTGCACGAAAGACCACTTTTGCCATTGGTCTTTG
1521 GGTACAGGCCACTAATACCAAAATATTTAGTTTGTGGCTACTTTTGCTTAAAGAGATAGAACTTCAGTCCAGAGGCCGGA
1601 TTGAAGTTCAGTCCTTAAAGATTGAACTTCGATCCAGTGCCATATGGACTGAAGTTCAGTCAAGTCCTTAAGATGGAACT
1681 TCAGTCCAGAGCCATATGGACTGAAGTTCAATCCTTAAAGATAGAACTTCAGTCCAGGGGCCGTATGGACTGAAGTTCAG
1761 TCAATTATCAGAACTTAAGTCAGTATTTATTTAGTAAAGGCCCAAAAGTGGTTAGTATAAGACCAATAAAAATAGAGGCC
1841 TAAAACTAAATAACAGTGTTAAAAGTGGCTGATGGACGAAATTTCTACAAAATGGACTCGAGGTAGCAATTCAACTTCAA
1921 CCTATGGTGTCATAGTCGTACAATTCTTCCAATCACCCCTACTAAGTGAAGTGAAGCGAAGATGATGAGAATTGCAGTGC
2001 GTTACTGTCTCAATGGTAATCCCTTTTTCTCATTCTTTGCTTATTCAATTGCACCCCGACATTATTCTACCAATACATGT
2081 TCCATTTCAGTTAAAGGGAATTTTGGGGTTTCTAATGAATTTGAGAATGTTAAGTGTTTAGATGATGCTTTCAGTTTGTT
2161 CCGTCAAATGGTTACAACTAAGCCTCTTCCTTCTGCTGTCTCTTTCTCTAAATTGTTGAAAGCTTTGGTACATATGAAGC
2241 ATTACTCTTCTGTTGTTTCTATTTTTCGAGAAATCCACAAATTACGTATTCCTGTTGATGCTTTCGCCTTGAGCACTGTG
2321 GTTAACAGTTGTTGCCTTATGCATCGTACCGATCTCGGATTTTCTGTATTAGCCATTCACTTCAAGAAAGGTATTCCATA
2401 TAATGAAGTCACCTTTACTACCTTAATAAGGGGACTTTTTGCTGAAAATAAGGTCAAAGATGCTGTTCATTTGTTCAAAA
2481 AGTTGGTGAGGGAGAATATATGTGAGCCTGATGAAGTCATGTATGGGACGGTCATGGATGGGCTTTGCAAGAAGGGCCAT
2561 ACTCAAAAAGCTTTTGATTTGCTCCGGTTAATGGAACAAGGAATTACTAAGCCCGATACATGCATCTACAACATTGTTAT
2641 CGATGCCTTTTGCAAAGATGGGATGCTAGATGGTGCTACCAGCCTTTTGAACGAGATGAAACAAAAAAACATTCCTCCAG
2721 ACATTATTACATATACCTCATTGATCGATGGTTTGGGTAAGTTAAGTCAGTGGGAAAAGGTTAGGACTTTGTTCCTTGAG
2801 ATGATACATCTTAATATTTATCCAGATGTGTGCACCTTCAACTCCGTCATTGATGGACTATGCAAAGAGGGGAAAGTTGA
2881 AGATGCCGAGGAAATAATGACATACATGATCGAAAAAGGTGTAGAACCTAATGAGATAACCTACAATGTGGTAATGGATG
2961 GATATTGCTTGCGTGGTCAAATGGGTAGAGCGAGGAGAATTTTTGATTCCATGATAGATAAGGGCATTGAGCCTGATATC
3041 ATTAGCTATACCGCACTAATAAATGGATACGTCGAGAAAAAGAAAATGGATAAGGCCATGCAATTGTTTCGTGAAATTTC
3121 TCAAAATGGATTGAAACCTAGTATTGTTACCTGCAGTGTTCTCTTGCGTGGTCTTTTTGAAGTTGGAAGAACTGAATGTG
3201 CAAAAATATTCTTTGATGAGATGCAAGCTGCGGGGCACATACCTAATTTATACACTCATTGCACTTTGCTTGGTGGTTAT
3281 TTTAAGAATGGACTTGTTGAAGAGGCTATGTCACACTTCCATAAGTTGGAAAGGAGGAGAGAAGATACAAATATTCAAAT
3361 TTACACGGCTGTCATTAATGGATTGTGCAAAAATGGTAAGCTCGACAAAGCTCATGCTACGTTTGAGAAGCTTCCCTTGA
3441 TAGGCTTACATCCTGATGTGATAACATACACTGCAATGATTAGTGGATATTGTCAAGAAGGGTTGTTAGATGAAGCTAAA
3521 GATATGCTAAGGAAAATGGAGGACAATGGTTGTTTGCCAGACAACCGAACATACAATGTTATTGTGCGGGGATTTTTCAG
3601 AAGCAGTAAAGTTAGTGAAATGAAGGCTTTTCTGAAGGAAATAGCTGGGAAGAGCTTCTCATTTGAGGCAGCTACTGTAG
3681 AGTTATTGATGGATATTATAGCAGAGGATCCTTCTTTGCTTAACATGATTCCAGAATTTCACCGGGATAATAAGAAGTGA
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3761 ATAACTTTTGCACCTGTTTTTTTTGACGATATCACCATTATTCTGCTATTTCCTTTCATCTTAGCAAAAGAAATTGCATC
3841 CAGTGGAATTGCGGAAGCTGAAAAAATGGCAAGAAGAACATTGCTTAAGCTTTCCTGGCAAGCTTATATCGGAGGGACAT
3921 CATTTTGGTTGTTTTGGCTCTCTTCTTTATCTTGGAAATCAAATGTTCTGCGCTCTTAATATCAGAAACAATGTGAACTC
4001 CCATATATGTACGAGTTATAAGTTTCGGAATATGATTTCAATGGTTTCAGTATTCTATTTTTGATATGGAATTAATTTTT
4081 GAGCGACCCAGTGTTGACCATTGCCTACCTTCGGTTATTATATGATTGAAATTCCCTCCAATCTCCAATACTCACTTCAT
4161 TTTGTCTTGTTGAATTTTTCAATTTTTCTTTTTCTGTTACGATTGTCATTTTCACCGCCTTGAGTATCCATCAGGTTCCA
4241 GTTGAAAAAGAATCATTTTTTGCCATGACCATCATGCTTTCTGAGTGCAAGATCAAGAGAGGTACTTTTCTCTCTAAGAA
4321 CCTCTTGGTTTTTTAAGTGTTCTGGGTTCTTTCAGTACTTTTAAGCTATTTTCTAATCCTTTGAAGAGATTCATACATAT
4401 CTGTGCATGTGTTTGTTTCTTTTTTTCGGGTGATACTTTGTTTTATAGCTAAGGATTGAAAAGGTAATTTTCATTTTCAT
4481 TAGCAATAGATATGAAACAGCTTTGTAAGGACTCTGGAGTCTCCTAAAAATTTTGGCTATGCAAATAGCCTATTGCATCA
4561 ATTTGTCGTTGAAATCCATGTATCATAAAAAAA
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Rf-PPR592, isolated from *Petunia* has an open reading frame ("ORF") of 1779 bp, extending between nucleotides 1982-3760.

[0042] The nucleic acid molecule of the present invention which has the nucleotide sequence of from nucleotide 1982 to 3760 of SEQ ID NO: 1 encodes a protein or polypeptide having a deduced amino acid sequence of SEQ ID NO: 2, as follows:

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MMRIAVRYCLNGNPFFSFFAYSIAPRHYSTNTCSISVKGNFGVSNEFENVKCLDDAFSLFRQMVTTKPLPSAVSFS
KLLKALVHMKHYSSVVSIFREIHKLRIPVDAFALSTVVNSCCLMHRTDLGFSVLAIHFKKGIPYNEVTFTTLIRGL
FAENKVKDAVHLFKKLVRENICEPDEVMYGTVMDGLCKKGHTQKAFDLLRLMEQGITKPDTCIYNIVIDAFCKDGM
LDGATSLLNEMKQKNIPPDIITYTSLIDGLGKLSQWEKVRTLFLEMIHLNIYPDVCTFNSVIDGLCKEGKVEDAEE
IMTYMIEKGVEPNEITYNVVMDGYCLRGQMGRARRIFDSMIDKGIEPDIISYTALINGYVEKKKMDKAMQLFREIS
QNGLKPSIVTCSVLLRGLFEVGRTECAKIFFDEMQAAGHIPNLYTHCTLLGGYFKNGLVEEAMSHFHKLERRREDT
NIQIYTAVINGLCKNGKLDKAHATFEKLPLIGLHPDVITYTAMISGYCQEGLLDEAKDMLRKMEDNGCLPDNRTYN
VIVRGFFRSSKVSEMKAFLKEIAGKSFSFEAATVELLMDIIAEDPSLLNMIPEFHRDNKK
```

[0043] As shown in Figure 1D, most of the predicted mature protein (87%) of Rf-PPR592 consists of 14 pentatricopeptide repeat motifs (PPRs). These repeats extend from the amino acid in position 54 to the amino acid in position 544 and are organized in two sets of tandem repeats, one set containing 3 PPRs from amino acid 54 to amino acid 158, the other set containing 11 PPRs from amino acid 160 to amino acid 544. Thus, another suitable nucleic acid molecule in accordance with the present invention encodes a protein containing a motif having an amino acid sequence corresponding to any of the PPR motifs (SEQ ID NOs: 3 to 18), where SEQ ID NO: 3 is as follows:

E E A . . L Y . . M . . . G . . P N . . T Y N A L I N A Y A K . G . .

where SEQ ID NO: 4 is as follows:

D . A . . . F . . M . . . G . . P D . . T Y . . L I . G L C K . G . .

where SEQ ID NO: 5 is as follows:

D D A F S L F R Q M V T T K P L P S A V S F S K L L K A L V H M K H Y

where SEQ ID NO: 6 is as follows:

S S V V S I F R E I H K L R I P V D A F A L S T V V N S C C L M H R T

where SEQ ID NO: 7 is as follows:

D L G F S V L A I H F K K G I P Y N E V T F T T L I R G L F A E N K V

where SEQ ID NO: 8 is as follows:

D A V H L F K K L V R E N I C E P D E V M Y G T V M D G L C K K G H T

where SEQ ID NO: 9 is as follows:

Q K A F D L L R L M E Q G I T K P D T C I Y N I V I D A F C K D G M L

where SEQ ID NO: 10 is as follows:

D G A T S L L N E M K Q K N I P P D I I T Y T S L I D G L G K L S Q W

where SEQ ID NO: 11 is as follows:

E K V R T L F L E M I H L N I Y P D V C T F N S V I D G L C K E G K V

where SEQ ID NO: 12 is as follows:

E D A E E I M T Y M I E K G V E P N E I T Y N V V M D G Y C L R G Q M

where SEQ ID NO: 13 is as follows:

G R A R R I F D S M I D K G I E P D I I S Y T A L I N G Y V E K K K M

where SEQ ID NO: 14 is as follows:

D K A M Q L F R E I S Q N G L K P S I V T C S V L L R G L F E V G R T

where SEQ ID NO: 15 is as follows:

E C A K I F F D E M Q A A G H I P N L Y T H C T L L G G Y F K N G L V

where SEQ ID NO: 16 is as follows:

E E A M S H F H K L E R R R E D T N I Q I Y T A V I N G L C K N G K L

where SEQ ID NO: 17 is as follows:

D K A H A T F E K L P L I G L H P D V I T Y T A M I S G Y C Q E G L L

and where SEQ ID NO: 18 is as follows:

D E A K D M L R K M E D N G C L P D N R T Y N V I V R G F F R S S K V

A PPR motif-containing gene can be identified if it contains the consensus sequence (SEQ ID NOs: 3 or 4) or if it is found with a MEME software (Bailey et al., "Fitting a Mixture Model by Expectation Maximization to Discover Motifs in Biopolymers," Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California (1994), which is hereby incorporated by reference in its entirety). To find whether a protein has a PPR motif with the MEME software, the parameters for motif searching should be set as minimum width=35, maximum width=35. MEME (Multiple Em for Motif Elicitation) is a software tool for discovering motifs in a group of related DNA or protein sequences (Bailey et al., "Fitting a Mixture Model by Expectation Maximization to Discover Motifs in Biopolymers," Proceedings of the Second

International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California (1994), which is hereby incorporated by reference in its entirety). MEME takes as input a group of DNA or protein sequences (the "training set") and outputs as many motifs as requested. MEME uses statistical modeling techniques to automatically choose the best width, number of occurrences, and description for each motif. MEME represents motifs as position-dependent letter-probability matrices which describe the probability of each possible letter at each position in the pattern. Individual MEME motifs do not contain gaps. Patterns with variable-length gaps are split by MEME into two or more separate motifs.

[0044] Another suitable nucleic acid molecule for the present invention is a nucleic acid molecule which encodes a protein having an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input. Meta-MEME is a software toolkit for building and using motif-based hidden Markov models of DNA and proteins. The input to Meta-MEME is a set of similar protein sequences, as well as a set of motif models discovered by MEME. Meta-MEME combines these models into a single, motif-based hidden Markov model and uses this model to produce a multiple alignment of the original set of sequences and to search a sequence database for homologs (Grundy et al., "Meta-MEME: Motif-based Hidden Markov Models of Biological Sequences," Computer Applications in the Biosciences, 13(4):397-406 (1997), which is hereby incorporated by reference in its entirety).

[0045] Also suitable for the present invention is a nucleic acid molecule which encodes a protein having an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input for comparison (Fulton et al., "Identification, Analysis, and Utilization of Conserved Ortholog Set Markers for Comparative Genomics in Higher Plants," Plant Cell, 14:1457-1467 (2002), which is hereby incorporated by reference in its entirety).

[0046] Also suitable in the present invention is a nucleic acid molecule which has a nucleotide sequence of SEQ ID NO: 19, an 8.5 kb fragment containing *Rf-PPR592* capable of transforming cytoplasmic male sterile plants, as follows:

GGATCCAAAATTTCACTAAAGGTTAAACGCGAGGATACTGAAGTTGGAGAGCAATGTGGTATCTTGGTGCATGGAC
GGAGTCATGGGGGTATAGTTGCTGGCTATTTAGCTAACTGGAGAACTGTTGTGAGGAATTATTTAAAGAATGCTAC
TTTCTCGTCCACATAAACATGTCCAAATATTTTCTACTTGATAGAGAGTTCAAGGAAATAGTGTGGATTTCTTCCC
AAACACAAACGATTTGAGAAAACTGAAGTGAAGGCTGAAGAGAAAACTAAAGAGAACTGGAAGCTAAGAAACACAG
AAGCACAAACCTATAAACATAGACACTGGCATGTTGCAGAAAATTTTAACTTTCGATTCTCCAGTAGAAAGACACA
AATACATCAGTAAATTTTCTTTAGGCTCAAGCAAGGATACATCTTGGTAGAATTTGCATTATACCAACATAATAAG
CTCAAAAAAATAACTAAGCTGCAACTAGCTACTTGGTCCGAGAAGCTTTTGCTATCAGGAAGTTCCACAGTTCCAA
AACCAAGGTAGACTATCAAGCTAGTTCCCACCAGTCATTTTCTTAGACTTTGCTCTCACGATAAACTAAGATCATT
TTTTTATGATACATGGATTTCAACGACAAATTGATGCAATAGGCTATTTGCATAGCCAAAATTTTTAGGAGACTCC
AGAGTCCTTACAAAGCTGTTTCATATCTATTGCTAATGAAAATGAAAATTACCTTTTCAATCCTTAGCTATAAAAC
AAAGTATCACCCGAAAAAAAGAAACAAACACATGCACAGATATGTATGAATCTCTTCAAAGGATTAGAAAATAGCT
TAAAAGTACTGAAAGAACCCAGAACACTTAAAAAACCAAGAGGTTCTTAGAGAGAAAAGTACCTCTCTTGATCTTG
CACTCAGAAAGCATGATGGTCATGGCAAAAAATGATTCTTTTTCAACTGGAACCTGATGGATACTCAAGGCGGTGA
AAATGACAATCGTAACAGAAAAAGAAAAATTGAAAAATTCAACAAGACAAAATGAAGTGAGTATTGGAGATTGGAG
GGAATTTCAATCATATAATAACCGAAGGTAGGCAATGGTCAACACTGGGTCGCTCAAAAATTAATTCCATATCAAA
AATAGAATACTGAAACCATTGAAATCATATTCCGAAACTTATAACTCGTACATATATGGGAGTTCACATTGTTTCT
GATATTAAGAGCGCAGAACATTTGATTTCCAAGATAAAGAAGAGAGCCAAAACAACCAAAATGATGTCCCTCCGAT
ATAAGCTTGCCAGGAAAGCTTAAGCAATGTTCTTCTTGCCATTTTTTCAGCTTCCGCAATTCCACTGGATGCAATT
TCTTTTGCTAAGATGAAAGGAAATAGCAGAATAATGGTGATATCGTCAAAAAAAACAGGTGCAAAAGTTATTCACT
TCTTATTATCCCGGTGAAATTCTGGAATCATGTTAAGCAAAGAAGGATCCTCTGCTATAATATCCATCAATAACTC
TACAGTAGCTGCCTCAAATGAGAAGCTCTTCCCAGCTATTTCCTTCAGAAAAGCCTTCATTTCACTAACTTTACTG
CTTCTGAAAAATCCCCGCACAATAACATTGTATGTTCGGTTGTCTGGCAAACAACCATTGTCCTCCATTTTCCTTA
GCATATCTTTAGCTTCATCTAACAACCCTTCTTGACAATATCCACTAATCATTGCAGTGTATGTTATCACATCAGG
ATGTAAGCCTATCAAGGGAAGCTTCTCAAACGTAGCATGAGCTTTGTCGAGCTTACCATTTTTGCACAATCCATTA
ATGACAGCCGTGTAAATTTGAATATTTGTATCTTCTCTCCTCCTTTCCAACTTATGGAAGTGTGACATAGCCTCTT
CAACAAGTCCATTCTTAAAATAACCACCAAGCAAAGTGCAATGAGTGTATAAATTAGGTATGTGCCCCGCAGCTTG
CATCTCATCAAAGAATATTTTTGCACATTCAGTTCTTCCAACTTCAAAAAGACCACGCAAGAGAACACTGCAGGTA
ACAATACTAGGTTTCAATCCATTTTGAGAAATTTCACGAAACAATTGCATGGCCTTATCCATTTTCTTTTTCTCGA
CGTATCCATTTATTAGTGCGGTATAGCTAATGATATCAGGCTCAATGCCCTTATCTATCATGGAATCAAAAATTCT
CCTCGCTCTACCCATTTGACCACGCAAGCAATATCCATCCATTACCACATTGTAGGTTATCTCATTAGGTTCTACA
CCTTTTTCGATCATGTATGTCATTATTTCCTCGGCATCTTCAACTTTCCCCTCTTTGCATAGTCCATCAATGACGG
AGTTGAAGGTGCACACATCTGGATAAATATTAAGATGTATCATCTCAAGGAACAAAGTCCTAACCTTTTCCCACTG
ACTTAACTTACCCAAACCATCGATCAATGAGGTATATGTAATAATGTCTGGAGGAATGTTTTTTTTGTTTCATCTCG
TTCAAAAGGCTGGTAGCACCATCTAGCATCCCATCTTTGCAAAAGGCATCGATAACAATGTTGTAGATGCATGTAT
CGGGCTTAGTAATTCCTTGTTCCATTAACCGGAGCAAATCAAAAGCTTTTTGAGTATGGCCCTTCTTGCAAAGCCC
ATCCATGACCGTCCCATACATGACTTCATCAGGCTCACATATATTCTCCCTCACCAACTTTTTGAACAAATGAACA
GCATCTTTGACCTTATTTTCAGCAAAAAGTCCCCTTATTAAGGTAGTAAAGGTGACTTCATTATATGGAATACCTT
TCTTGAAGTGAATGGCTAATACAGAAAATCCGAGATCGGTACGATGCATAAGGCAACAACTGTTAACCACAGTGCT
CAAGGCGAAAGCATCAACAGGAATACGTAATTTGTGGATTTCTCGAAAAATAGAAACAACAGAAGAGTAATGCTTC
ATATGTACCAAAGCTTTCAACAATTTAGAGAAAGAGACAGCAGAAGGAAGAGGCTTAGTTGTAACCATTTGACGGA
ACAAACTGAAAGCATCATCTAAACACTTAACATTCTCAAATTCATTAGAAACCCCAAAATTCCCTTTAACTGAAAT
GGAACATGTATTGGTAGAATAATGTCGGGGTGCAATTGAATAAGCAAAGAATGAGAAAAAGGGATTACCATTGAGA
CAGTAACGCACTGCAATTCTCATCATCTTCGCTTCACTTCACTTAGTAGGGGTGATTGGAAGAATTGTACGACTAT
GACACCATAGGTTGAAGTTGAATTGCTACCTCGAGTCCATTTTGTAGAAATTTCGTCCATCAGCCACTTTTAACAC

TGTTATTTAGTTTTAGGCCTCTATTTTTATTGGTCTTATACTAACCACTTTTGGGCCTTTACTAAATAAATACTGA
CTTAAGTTCTGATAATTGACTGAACTTCAGTCCATACGGCCCCTGGACTGAAGTTCTATCTTTAAGGATTGAACTT
CAGTCCATATGGCTCTGGACTGAAGTTCCATCTTAAGGACTTGACTGAACTTCAGTCCATATGGCACTGGATCGAA
GTTCAATCTTTAAGGACTGAACTTCAATCCGGCCTCTGGACTGAAGTTCTATCTCTTTAAGCAAAAGTAGCCACAA
ACTAAATATTTTGGTATTAGTGGCCTGTACCCAAAGACCAATGGCAAAAGTGGTCTTTCGTGCACTTTCCCCGTCC
ATTTTGCTAAATCATACAAAAGATCATAACCGAGATAAGGAGGTATATATTGTGAAATTTTTTGGAACTTGAATAA
TTGTGGGCTGAACTTCAGCCTACTTTGCGAATGGGTAAAAGTGCATGAGAGACCACTTTTTTTTGCAGATTTTGCT
TGAGAGGTCATTTTTTGAAACTTTAATCCTTGTGGGTTGAACTTCACACAAGTTCAGCCCACAAGGATTGAAGTTC
AACTTCAGGCCACCATAAGGGGCGAAGTTCAACTTCAGTCCACAAGGTTGAAGTTTACGCATCTATGCCTAAAAAT
TCAGCCCTTACGGATTGAAGTTGAACTTAATAACTTAGGCATGAAGTTCAAGCGCACAAAGATTGAAGTTCCAAAA
AGTGGTCTCTCATGTAAAACCAATAAAAAAATGACTTCAAACCAAATACTAGTGGTAAAAGTGGCCTGTGAGCTAA
TTTTTTACTTGTGAATGTATGAAGTTCGGCCCACAAGGTCTGAAGTTCGGCCCACAATGATTAAAGTTCCAAAAAA
GCTAAAAACTAGCTCTTTTTCTTTGAAAGTAGCTTCAACGGTAAAGGCAAGCCAAAAAGTGGCTTTTCCTTGCACT
TTTCCTTAAGTTTATAATGAATAAATATCGAATGGAAATACAATCTTATAGTGATGCCCATTTCTCACTCCCTAAG
GCAGCATTGTCTTTGACTGCCTTTTGCTTAAGCAATATTTGCTTTTGAATTTCTTCCTACATTTTTCTACATAATT
TGACGTGTTGTCTAGGCAACACTTGTCCGTACAATCTTTTCGAATACTTTCCCAGACAACACTTCTTTTAACGTAA
AAATTTGGCCATGTAGTCTATTTGCCCCTCGCTAAATGAAAACTAGCCAGCATTTCAAAATTTTTAGAAGACCAGC
CAAAATCAAGAAACATATAAATATTTCAGTTTTTTGTACTATGACTTGAACTACAATTTTCAAAAAGAATGTTTTT
AAAACTACCCAGCTTACACTAAAAAATTACACTACCATCACTCAAATTTTGTTTAAACATTTTATAGCCACACAAC
CACAACATTGGGGTACACTATTGCGGTGTCAAACTTGTATACTATTGGGGGTATACGAATACTAAAAAGGTAAATA
ATAGAAGATATCGTATAGGTATACTGTCGCTATGGGATATACAAGCTTGGAGTATATGCGACTATAAAATAAAATA
TTTTTAGCCAAATGGCCGACTCAGGTAAATATTTTTAGGAAATATTACACCACATGACTACCTAATAGCTATATTA
CAAAAAATAACAATATTTTTATCATATTTACAATACATAACAATGAGTTTTGTATATATTATGTAAAAAAATTATT
GTTATTTTTTGTAAAGATAACATTATTAGCGGAGCTACCCTTTTTCAAGGGTATGTAAATATAACACTGTGCAAAT
AGACAGAAAAAATCAGTTTGTATATATATATCAGATATTGATTCCCCCTTCATTTTTTCGTATGTTTACTTTTTTA
TATTTATATATCCCTTAGTAAAAATACTGGCTCCGCCACTGCCAGTAAGGTAGTATTAGTTTGCGTCGCTCAATAA
AGTAACATCTATCGTTTATTTTTCATCAACATTAAAAAGGAAGATTCACTATCCACATAGGCATCATCATTATCAA
AGAATATCAGTTCATACATTGTATATATATAACTTTCTCAAATAAACTAACTTTAAAATGAAGTACATTAAAAAGG
AAGATTCACTATCCTTTTAATATTTCGTATATTTACTTATTTATATTTTGATACTCCTTAGTAAAAATACTGGCTC
CGCCACTACCAGTGATGTAATATTAATTCGCGTCCCTCACTAAAGTAACACCTATAATTTAATTTTCATGAAGTCA
GAGTTAGCATTGGAAAGGGATATAAGCACATGCATTGTGTATATATATATAACTTGCTCAAATAAACTAACTTAAA
AATGAAATTTTACTTTTCCTAGTACAATGAACTATGCATCAATGCGTAATTAGTTGAGGTCGGCTATATGAATATG
TTATTAATTTGAAAGCAAAACATAATAACTGATAGAAGAATTTTGCACCTAAAAATTGAACTTGAGCTGCTTCAGT
TACTATCTCATTTTTCACTATATATGTGTGTATCAGCTAATTCTATGATTTAATTAAACAAATTGTAAGTATTAAC
AAAATAACGAATAAATATGGAAAATAAGTACTTGATGAACGTAGGGCCGGAGTTGGCCGAGGTGACCGGAGACAAT
GGAAAGCAGAGTTACTATTTTTGACTAAATAGCCACAAAAGAATCATTGTTTTTACAATGTAGCAAGTTGGCACGA
TTATGATTCTTGACACAATAGCCACATTATAGAAAGATAATGTGGCACTAATGAGGTAATTTTCATTATGGAATGA
TAACAAACAAATAAGTACACGATTAAAACAAACTGAAAGGGTTTTGCGCGATAATTTAATCATTGTTTTACGAAAA
TACTCATCAAAATCAAAATATTTATCTGCCTCTGCATGTAAGTTTCATATTTACTCGTCTTGCCATAATTTATATG
AAAAAATTTACTCACACCGGATATATATACCTAACCATAGCAATTAACTATGGTAATGTGATGTAATGAAGAGAGA
ATGTCTATTAATTAATTATGGCTAAGTGATAGTAGTGTATTGTAAACAAATGACGTGCATTTGTTGATTAGACACT
TACAAAAATACCCACGAAATCTAAAATAATTACAGCCACTATCCACTACTTTCAAATATTATCTGGCCTACCCATT
AAAATATTTACTCACTCTACCCCTCCAGACTTATATATTATAAGGTATAAAAAGGTAAACAATAATAAATGGTCCT
CCAGACTTTTATACCATAATTTATGCAGCCTTAAAGGTATACACCTATAAACAAAGGTATACAATAAAAAATGGGT

ATGTTGGGTAAATACTTTTAGTTTTATGGGTAGAGTAATTTTTAATGGGTATGACTTGTAAATACTTTAAATTTCA
TGGGTATAGAGTGTAAAAATTCCTTTGTTGATTGGGTATATACACCCGATGTGGGTAAGTACTTGCCTAATTTTTG
CCCTAAGGTAAATATAGACTTATAGTATAAAAAAAAATACGCAGTGTGATAGATACTTTGAATTTCATGAGTAATG
TAATTTTTAATAGGTATAGTAAGGTAAATACTTTATATTCCAAGGGTACACATTGTAAAAAGCTCAATATTTTATT
CCAAAGAATAAGAGACCAAACAATGTGTTTGAGATTTATTACTTTGTTGTCCACCAAACTAAAAAGAAAACTTTAG
AAGTCTAAATTACAATAATCTTAACATGCATTTTACGAATAAATATCACAAAATCTCAAACTATTAGAGATAATGT
CGTGGATGATGTTAACATATTGGACTACACAACCCATTGTACAATAATTTTGAAGCATGTATATGCACGACCAAGA
CTCCATCATCATAGATCAAATGAATGTTCATTTTAATGCATGAAACCTAAGTAGAACATTTATGCCTTAATGAACT
AAAACCAAGCAAAAAGATACATCTACTTGTGCAATTGAATGAATTCTACCGTATATACTAATATACACCAGAGGTT
AGTTTAACACTTGGAACTTCAAAAGGTGTACAACCATAGAGTTTCCTTTACATTGATGGTTTCTTTCATTTCACTA
ACTGATAAAATGAAGGCTGGTATAGTCTACCAAATCCCTAGTTCCCTGTGAACTTGCATCCCTTCTAGCTACATGC
AGAACATGTCCTTTAGATCCCATAGGTGTATTGCCATTTGCCACTGAACAATGGAGGACAATGTATAATTGTCCTC
CTCACCCATTGCACATACTCTGTCATTTGCTGCACATCTACATGCCTTTTCTGAATATTCTTCTGAGTCAAATAAG
CATCATGAGACATCTGTCAAGTATCTTTGAATGGGATAATCACATTTCCAAATCGAAAGGTTCTTGTCTTAACAAG
TCAAGCTGCATCTCGACAAAGAGACTTCGTTGATGAAATGCGACCATAAAGAGCACATGCAAACCAGTTGTTAAAA
GCATTGTACACATATACCTACTTCTGATGTGAATAAAAGAAAGTCGATCAATGACAGAGGAAAACAGTCAATCTAT
AACCACAAAAATACTTTTCTTTAAAAGTACGACCACATAGATAACTATAATTTCCCGTAGATGTCAAACTCTTATT
GAATAAAAAATAAACAAACATGTACTATTTGCTCATTTATCCGACTGTCACAAGGATTTTCTTAATGATGGTATAA
TAGGAGCAATCCCTTTTATGACAGATGCACTAATTTGTTTGGGTGCATATTTCAATGCAGAACTGTGGGGTATATA
ATCTAAAATATCATTCAAATCAAACCTGGGAACGATTGAGAGAAGATTAGCATGGCCTCTGCACAAGGATGACACG
CATAAATCGAGAAATGTTCCAAATAAAGGAAATATATATATTACCTGTTTCAATTGGCATAGTTCTTAAAGAAGTT
TTGGCAGTTAAAGTATTAATAGTTTACCTTGTTTCGATTGTGGGATTTAGCCTTGGGGTTGTCTGGGACGGACCTG
TGATTATTCTGCTAATCTCCTTGTATATTCATGCAATGTGCAGTTTAATCCAGTGCATTTTGCGTGTTATGGATGG
ATCC

[0047] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr1*, which has a nucleotide sequence of SEQ ID NO: 20, as follows:

ATGGCGCGCCGCGTCCCTACCCGCCCGCGCGGCGGTGGCGGCGGCGGCGTCCCACGCTCGGAGGGCTCGATCCAAG
GGCGAGGAGGCCGCGCGGGGGGCAGTGGCGCCGAGGACGCACGCCACGTGTTCGACGAATTGCTCCGGCGTGGCAG
GGGCGCCTCGATCTACGGCTTGAACCGCGCCCTCGCCGACGTCGCGCGTCACAGCCCCGCGGCCGCCGTGTCCCGC
TACAACCGCATGGCCCGAGCCGGCGCCGGCAAGGTAACTCCCACCGTGCACACCTATGCCATCCTCATCGGCTGCT
GCTGCCGTGCGGGCCGCTTGGACCTCGGTTTCGCGGCCTTGGGCAATGTCGTCAAGAAGGGATTTAGAGTGGATGC
CATCACCTTCACTCCTCTGCTCAAGGGCCTCTGTGCCGACAAGAGGACGAGCGACGCAATGGACATAGTGCTCCGC
AGAATGACCGAGCTCGGCTGCATACCAGATGTCTTCTCCTACAATAATCTTCTCAAGGGTCTGTGTGATGAGAACA
GAAGCCAAGAAGCTCTCGAGCTGCTGCACATGATGGCTGATGATCGAGGAGGAGGTAGCCCACCTGATGTGGTGTC
GTATAACACTGTCCTCAATGGCTTCTTCAAAGAGGGGGATTCAGACAAAGCTTACAGTACATACCATGAAATGCTG
GACCGGGGGATTTTACCAGATGTTGTGACCTACAGCTCTATTATTGCTGCGTTATGCAAGGCTCAAGCTATGGACA
AAGCCATGGAGGTACTTAACACCATGGTTAAGAATGGTGTCATGCCTGATTGCATGACATATAATAGTATTCTGCA
TGGATATTGCTCTTCAGGGCAGCCAAAAGAGGCTATTGGAACACTCAAAAAGATGCGCAGTGATGGCGTCGAACCA
AATGTTGTTACTTATAGTTCACTGATGAATTATCTTTGCAAGAATGGAAGATCCACCGAAGCTAGAAAGATTTTCG
ATTCTATGACCAAGAGGGGCCTAGAGCCTGATATTGCTACCTATCGTACCCTGCTTCAGGGGTATGCTACCAAAGG

AGCCCTTGTTGAGATGCATGCTCTCTTGGATTTGATGGTACGAAATGGTATCCAACCGGATCATCATGTATTCAAC
ATTCTAATATGTGCATACGCTAAACAAGAGAAAGTAGATCAGGCAATGCTTGTATTCAGCAAAATGAGGCAGCATG
GATTGAATCCGAATGTAGTGTGCTATGGAACAGTTATAGATGTACTTTGCAAGTCAGGCAGTGTAGATGATGCTAT
GCTTTATTTTGAGCAGATGATCGATGAAGGACTAACCCCTAACATTATTGTGTATACCTCCCTAATTCATGGTCTG
TGCACCTGTGACAAATGGGACAAGGCTGAAGAGTTAATTCTTGAAATGTTGGATCGAGGCATCTGTCTGAACACTA
TTTTCTTTAATTCAATAATTGACAGTCATTGCAAAGAAGGGAGGGTTATAGAATCTGAAAAACTCTTTGACTTGAT
GGTACGAATTGGTGTGAAGCCCGATATCATTACGTACAATACACTCATCGATGGATGCTGCTTAGCTGGTAAGATG
GATGAAGCAACGAAGTTACTTGCCAGCATGGTCTCAGTTGGGGTGAAACCTGATATTGTTACCTATGGCACCTTGA
TTAATGGCTACTGTAGAGTTAGCAGGATGGATGACGCATTAGCTCTTTTCAAAGAGATGGTGAGCAGTGGTGTTAG
TCCTAATATTATTACGTATAACATAATTCTGCAAGGTTTATTTCATACCAGAAGAACTGCTGCTGCAAAAGAACTC
TATGTCAGTATTACCAAAAGTGGAACACAGCTTGAACTTAGCACGTACAACATAATCCTTCATGGACTTTGCAAAA
ACAATCTCACTGACGAGGCACTTCGAATGTTTCAGAACCTATGTTTGACGGATTTACAGCTGGAGACTAGGACTTT
TAACATTATGATTGGTGCCTTACTTAAATGTGGAAGAATGGATGAAGCTAAGGATTTGTTTGCTGCTCACTCGGCT
AACGGTTTAGTGCCAGATGTTAGGACCTACAGTTTAATGGCAGAAAATCTTATAGAGCAGGGGTCGCTAGAAGAAT
TGGATGATCTATTTCTTTCAATGGAGGAGAATGGCTGTTCCGCCGACTCCCGCATGCTAAATTCCATTGTTAGGAA
ACTGTTACAGAGGGGTGATATAACCAGGGCTGGCACTTACCTGTTCATGATTGATGAGAAGCACTTCTCCCTCGAA
GCATCCACTGCTTCCTTCTTGTTAGAATCTTCCCCAATCGTCTGGGAGCAAATATCAAGAATATCACACTTGTCTG
TAAATTTGAAATTAATTAAGCAGCCCAAATGCACCTGTGAGTTAGGCCCAAAGTGGTCCCAAAATCTGCCTAAACC
TGGCACAAATTCGGTCGGTAGTGTCGCACAGTTTCACTTATCGCGCGGCGGTTATCGCGCTTACCGCGGGGGTACG
ACGGTTACCGCACTACCGCAGGGTGACGGTAACCCCGGCCCAAACGATAAGGTAAACCCTGGTCGCACAAATTTGG
CCCAAAACCGACCAGTTATCGCGCTACCGCGGGATGCCTCAGTAGGACCTTAG

Rhpr1 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0048] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 20 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 21 as follows:

MARRVPTRPRGGGGGGVPRSEGSIQGRGGRAGGSGAEDARHVFDELLRRGRGASIYGLNRALADVARHSPAAAVSR
YNRMARAGAGKVTPTVHTYAILIGCCCRAGRLDLGFAALGNVVKKGFRVDAITFTPLLKGLCADKRTSDAMDIVLR
RMTELGCIPDVFSYNNLLKGLCDENRSQEALELLHMMADDRGGGSPPDVVSYNTVLNGFFKEGDSDKAYSTYHEML
DRGILPDVVTYSSIIAALCKAQAMDKAMEVLNTMVKNGVMPDCMTYNSILHGYCSSGQPKEAIGTLKKMRSDGVEP
NVVTYSSLMNYLCKNGRSTEARKIFDSMTKRGLEPDIATYRTLLQGYATKGALVEMHALLDLMVRNGIQPDHHVFN
ILICAYAKQEKVDQAMLVFSKMRQHGLNPNVVCYGTVIDVLCKSGSVDDAMLYFEQMIDEGLTPNIIVYTSLIHGL
CTCDKWDKAEELILEMLDRGICLNTIFFNSIIDSHCKEGRVIESEKLFDLMVRIGVKPDIITYNTLIDGCCLAGKM
DEATKLLASMVSVGVKPDIVTYGTLINGYCRVSRMDDALALFKEMVSSGVSPNIITYNIILQGLFHTRRTAAAKEL
YVSITKSGTQLELSTYNIILHGLCKNNLTDEALRMFQNLCLTDLQLETRTFNIMIGALLKCGRMDEAKDLFAAHSA
NGLVPDVRTYSLMAENLIEQGSLEELDDLFLSMEENGCSADSRMLNSIVRKLLQRGDITRAGTYLFMIDEKHFSLE
ASTASFLLESSPIVWEQISRISHLSVNLKLIKQPKCTCELGPKWSQNLPKPGTNSVGSVAQFHLSRGGYRAYRGGT
TVTALPQGDGNPGPNDKVNPGRTNLAQNRPVIALPRDASVGP

[0049] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr2*, which has a nucleotide sequence of SEQ ID NO: 22, as follows:

ATGGCGCGCCGCGCCGCTTCCCGCGTCCGCGCCGGCGCTGTTGGCGCCCTTCGCTCGGAGGGCTCGACCCAAGGGC
GAGGGGGCCGCACGGGGGGCAGTGGCGCCGAGGACGCACGCCACGTGTTCGACGAATTGCTCCGGCGTGGCAGGGG
CGCCTCGATCTACGGCTTGAACTGCGCCCTCGCCGACGTCGCGCGTCACAGCCCCGCGGCCGCCGTGTCCCGCTAC
AACCGCATGGCCCGAGCCGGCGCCGACGAGGTAACTCCCAACTTGTGCACCTACGGCATTCTCATCGGTTCCTGCT
GCTGCGCGGGCCGCTTGGACCTCGGTTTCGCGGCCTTGGGCAATGTCATTAAGAAGGGATTTAGAGTGGACGCCAT
CGCCTTCACTCCTCTGCTCAAGGGCCTCTGTGCTGACAAGAGGACGAGCGACGCAATGGACATAGTGCTCCGCAGA
ATGACCCAGCTTGGCTGCATACCAAATGTCTTCTCCTACAATATTCTTCTCAAGGGGCTGTGTGATGAGAACAGAA
GCCAAGAAGCTCTCGAGCTGCTCCAAATGATGCCTGATGATGGAGGTGACTGCCCACCTGATGTGGTGTCGTATAC
CACTGTCATCAATGGCTTCTTCAAGGAGGGGGATCTGGACAAAGCTTACGGTACATACCATGAAATGCTGGACCGG
GGGATTTTACCAAATGTTGTTACCTACAGCTCTATTATTGCTGCGTTATGCAAGGCTCAAGCTATGGACAAAGCCA
TGGAGGTACTTACCAGCATGGTTAAGAATGGTGTCATGCCTAATTGCAGGACGTATAATAGTATCGTGCATGGGTA
TTGCTCTTCAGGGCAGCCGAAAGAGGCTATTGGATTTCTCAAAAAGATGCACAGTGATGGTGTCGAACCAGATGTT
GTTACTTATAACTCGCTCATGGATTATCTTTGCAAGAACGGAAGATGCACGGAAGCTAGAAAGATGTTCGATTCTA
TGACCAAGAGGGGCCTAAAGCCTGAAATTACTACCTATGGTACCCTGCTTCAGGGGTATGCTACCAAAGGAGCCCT
TGTTGAGATGCATGGTCTCTTGGATTTGATGGTACGAAACGGTATCCACCCTAATCATTATGTTTTCAGCATTCTA
ATATGTGCATACGCTAAACAAGGGAAAGTAGATCAGGCAATGCTTGTGTTCAGCAAAATGAGGCAGCAAGGATTGA
ATCCGGATACAGTGACCTATGGAACAGTTATAGGCATACTTTGCAAGTCAGGCAGAGTAGAAGATGCTATGCGTTA
TTTTGAGCAGATGATCGATGAAAGACTAAGCCCTGGCAACATTGTTTATAACTCCCTAATTCATAGTCTCTGTATC
TTTGACAAATGGGACAAGGCTAAAGAGTTAATTCTTGAAATGTTGGATCGAGGCATCTGTCTGGACACTATTTTCT
TTAATTCAATAATTGACAGTCATTGCAAAGAAGGGAGGGTTATAGAATCTGAAAAACTCTTTGACCTGATGGTACG
TATTGGTGTGAAGCCCGATATCATTACGTACAGTACTCTCATCGATGGATATTGCTTGGCAGGTAAGATGGATGAA
GCAACGAAGTTACTTGCCAGCATGGTCTCAGTTGGAATGAAACCTGATTGTGTTACATATAATACTTTGATTAATG
GCTACTGTAAAATTAGCAGGATGGAAGATGCGTTAGTTCTTTTTAGGGAGATGGAGAGCAGTGGTGTTAGTCCTGA
TATTATTACGTATAATATAATTCTGCAAGGTTTATTTCAAACCAGAAGAACTGCTGCTGCAAAAGAACTCTATGTC
GGGATTACCGAAAGTGGAACGCAGCTTCAACTTAGCACATACAACATAATCCTTCATGGGCTTTGCAAAAACAATC
TCACTGACGAGGCACTTCGAATGTTTCAGAACCTATGTTTGACGGATTTACAGCTGGAGACTAGGACTTTTAACAT
TATGATTGGTGCATTGCTTAAAGTTGGCAGAAATGATGAAGCCAAGGATTTGTTTGCAGCTCTCTCGGCTAACGGT
TTAGTGCCAGATGTTAGGACCTACAGTTTAATGGCAGAAAATCTTATAGAGCAGGGGTTGCTAGAAGAATTGGATG
ATCTATTTCTTTCAATGGAGGAGAATGGCTGTACTGCCAACTCCCGCATGCTAAATTCCATTGTTAGGAAACTGTT
ACAGAGGGGTGATATAACCAGGGCTGGCACTTACCTGTTCATGATTGATGAGAAGCACTTCTCCCTCGAAGCATCC
ACTGCTTCCTTGTTTTTAGATCTTTTGTCTGGGGGAAAATATCAAGAATATCATAGTTGTATTAGAGGAGGGATCT
TCTCTTTATGTGTAAATAGCGAGGTTCAAGAAAATCATTTGTTGGATTCAGAATCTGGTGTCCATTTTCTTCTTAA
ATTATTAAATCCTCCAGTGAATCTTGTTGATTCCAAAGCACCATCGATAGGTTCCAAACTTCTTGGAATCAGTAAA
GTTCAAATGCTTAATGGATCAAATAAGGATTCTGACTGCATTTCAGAGGAAATCCTTTCAAAAGTTGAAGAGATTC
TCTTAAGCTGTCAAGTGATCAAGTCGCTCGACAAAGATGACAAGAAAACAACAAGGCCAGAACTGTGTCCAAAGTG
GCTTGCTTTGTTGACAATGGAAAATGCATGCTTGTCTGCTGTTTCAGTAGAGGAGACTTCTGACACAGTGTCCAGA
GTTGGAGGAAATTTTAAAGAGACATTAAGGGAGATGGGAGGTCTTGATAGTATTTTTGACGTTATGGTGGATTTTC
ATTCAACATTGGAGAATCTCATAAAGGATACATCCACTTCAGCTTTGGACCGAAATGAAGGAACATCTTTGCAAAG
TGCTGCTCTCCTCTTGAAATGTTTGAAAATATTGGAAAATGCCATATTTCTAAGCGATGATAACAAGACCCATTTG

CTTAATATGAGTAGAAAATTGAACCCGAAACGCTCCTTGCTTTCTTTTGTTGGTGTCATTATCAATACTATTGAGT
TATTATCAGCTCTTTCAATACTTCAGAATTCTTCTGTTGTTTCCAGCTCTACATATCCGAAATCGTCTAAAGTCTC
TCAACAGAGTTACTCTGTGGTGATGGCGGGGGGCGACCGTGGCCGAGGCGTGGAGTGCCATCCGCATCAGGGTGTA
TCGGCCGCGCTGCTCCGCCCTGGTCCGCAGGCTTTGGCGGCGAGCTGGCGGCGGAGGGAGACTGTGGTGAGATCGG
ATTTCGCCGCTGGTGGTGTCGCTACCATGGGGGATTCGCCGCAGGCGCTCTCAGATCGGTTATGCGGGAGCGCAAC
AAAAGTATGGCGTGGCGGCGCGGAGTGGACGGCCGAGGCGTTCGCGCGGAATGGGGCTGCGGGACCGAGCCAGTCT
CGCTTGCCGGTAACGCGGAACCGAGCTCAGCACTACATTGCAAAGATTTGGGCAACTCTGACAATTTCCATGTTCT
ACAAGCTTGACGTCGAGGGAATGGAGAACCTGCCACCGAATAGTAGCCCTGCTATCTATGTTGCGAACCATCAGAG
TTTTTTGGATATCTATACCCTTCTAACTCTAGGAAGGTGTTTCAAGTTTATAAGCAAGACAAGTATATTTATGTTC
CGAATTATTTGA

Rhpr2 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0050] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 22 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 23 as follows:

MARRAASRVRAGAVGALRSEGSTQGRGGRTGGSGAEDARHVFDELLRRGRGASIYGLNCALADVARHSPAAAVSRY
NRMARAGADEVTPNLCTYGILIGSCCCAGRLDLGFAALGNVIKKGFRVDAIAFTPLLKGLCADKRTSDAMDIVLRR
MTQLGCIPNVFSYNILLKGLCDENRSQEALELLQMMPDDGGDCPPDVVSYTTVINGFFKEGDLDKAYGTYHEMLDR
GILPNVVTYSSIIAALCKAQAMDKAMEVLTSMVKNGVMPNCRTYNSIVHGYCSSGQPKEAIGFLKKMHSDGVEPDV
VTYNSLMDYLCKNGRCTEARKMFDSMTKRGLKPEITTYGTLLQGYATKGALVEMHGLLDLMVRNGIHPNHYVFSIL
ICAYAKQGKVDQAMLVFSKMRQQGLNPDTVTYGTVIGILCKSGRVEDAMRYFEQMIDERLSPGNIVYNSLIHSLCI
FDKWDKAKELILEMLDRGICLDTIFFNSIIDSHCKEGRVIESEKLFDLMVRIGVKPDIITYSTLIDGYCLAGKMDE
ATKLLASMVSVGMKPDCVTYNTLINGYCKISRMEDALVLFREMESSGVSPDIITYNIILQGLFQTRRTAAAKELYV
GITESGTQLELSTYNIILHGLCKNNLTDEALRMFQNLCLTDLQLETRTFNIMIGALLKVGRNDEAKDLFAALSANG
LVPDVRTYSLMAENLIEQGLLEELDDLFLSMEENGCTANSRMLNSIVRKLLQRGDITRAGTYLFMIDEKHFSLEAS
TASLFLDLLSGGKYQEYHSCIRGGIFSLCVNSEVQENHLLDSESGVHFLLKLLNPPVNLVDSKAPSIGSKLLGISK
VQMLNGSNKDSDCISEEILSKVEEILLSCQVIKSLDKDDKKTTRPELCPKWLALLTMENACLSAVSVEETSDTVSR
VGGNFKETLREMGGLDSIFDVMVDFHSTLENLIKDTSTSALDRNEGTSLQSAALLLKCLKILENAIFLSDDNKTHL
LNMSRKLNPKRSLLSFVGVIINTIELLSALSILQNSSVVSSSTYPKSSKVSQQSYSVVMAGGDRGRGVECHPHQGV
SAALLRPGPQALAASWRRRETVVRSDFAAGGVATMGDSPQALSDRLCGSATKVWRGGAEWTAEAFARNGAAGPSQS
RLPVTRNRAQHYIAKIWATLTISMFYKLDVEGMENLPPNSSPAIYVANHQSFLDIYTLLTLGRCFKFISKTSIFMF
RII

[0051] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr3*, which has a nucleotide sequence of SEQ ID NO: 24, as follows:

ATGGCGCGCCGCGCCGCTTCCCGCGCTGTTGGCGCCCTTCGCTCGGACGGCTCGATCCAAGGGCGAGGAGGCCGCG
CGGGGGGCAGTGGCGCCGAGGACGCACGCCACGTGTTCGACGAATTGCTCCGGCGTGGCAGGGGCGCCTCGATCTA

CGGCTTGAACCGCGCCCTCGCCGACGTCGCGCGTCACAGCCCCGCGGCCGCCGTGTCCCGCTACAACCGCATGGCC
CGAGCTGGCGCCGACGAGGTAACTCCCGACTTGTGCACCTACGGCATTCTCATCGGTTGCTGCTGCCGCGCGGGCC
GCTTGGACCTCGGTTTCGCGGCCTTGGGCAATGTCATTAAGAAGGGATTTAGAGTGGAAGCCATCACCTTCACTCC
TCTGCTCAAGGGCCTCTGTGCCGACAAGAGGACGAGCGACGCAATGGACATAGTGCTCCGCAGAATGACCGAGCTC
GGTTGCATACCAAATGTCTTCTCCTACAATAATCTTCTCAACGGGCTGTGTGATGAGAACAGAAGCCAAGAAGCTC
TCGAGTTGCTGCACATGATGGCTGATGATCGAGGAGGAGGTAGCCCACCTGATGTGGTGTCGTATACCACTGTCAT
CAATGGCTTCTTCAAAGAGGGGGATTCAGACAAAGCTTACAGTACATACCATGAAATGCTGGACCGGGGGATTTTA
CCTGATGTTGTGACCTACAGCTCTATTATTGCTGCGTTATGCAAGGGTCAAGCTATGGACAAGCCATGGAGTCATT
GCAAAGAAGGGAGGGTTATAGAATCTGAAAAACTCTTTGACCTGATGGTACGTATTGGTGTGAAGCCTGATATCAT
TACATACAGTACACTCATCGATGGATATTGCTTGGCAGGTAAGATGGATGAAGCAATGAAGTTACTTTCTGGCATG
GTCTCAGTTGGGTTGAAACCTAATACTGTTACTTATAGCACTTTGATTAATGGCTACTGCAAAATTAGTAGGATGG
AAGACGCGTTAGTTCTTTTTAAGGAGATGGAGAGCAGTGGTGTTAGTCCTGATATTATTACGTATAACATAATTCT
GCAAGGTTTATTTCAAACCAGAAGAACTGCTGCTGCAAAAGAACTCTATGTCAGGATTACCGAAAGTGGAACGCAG
ATTGAACTTAGCACATACAACATAATCCTTCATGGACTTTGCAAAAACAAACTCACTGATGATGCACTTCAGATGT
TTCAGAACCTATGTTTGATGGATTTGAAGCTTGAGGCTAGGACTTTCAACATTATGATTGATGCATTGCTTAAAGT
TGGCAGAAATGATGAAGCCAAGGATTTGTTTGTTGCTTTCTCGTCTAACGGTTTAGTGCCGAATTATTGGACGTAC
AGGTTGATGGCTGAAAATATTATAGGACAGGGGTTGCTAGAAGAATTGGATCAACTCTTTCTTTCAATGGAGGACA
ATGGCTGTACTGTTGACTCTGGCATGCTAAATTTCATTGTTAGGGAACTGTTGCAGAGAGGAGTAGTGGTGGTGGT
GAGTGGTGAATCTGCCACCACCCCACCACCAACTCTCAAAATTCTGACATGTGGGATCACTGTCAATCCCTTCTCC
AAGACATGTGGGATCACTGTCAATCCCTTCTCCAAACCAATTGTGCAGACAGGTGCTTGCGGTCAGGTTAAAGAAG
TTGGCAAAAATGCTTCTGAAGAAAGGTTAATTGTTGTTTCATCTCAGGAGATTCCAGATGATCCAGTGTCTCCAAC
AATTGAGGCGCTTATTTTGCTCCATAGTAAAGCAAGTACACTTGCTGAGAACCACCAGTTGACAACACGGCTTGTT
GTACCATCAAACAAAGTTGGTTGTATTCTTGGGGAAGGTGGAAAGGTAATTACTGAAATGAGAAGACGGACTGGGG
CTGAAATCCGAGTCTACTCAAAAGCAGATAAACCTAAGTACCTGTCTTTTGATGAGGAGCTTGTGCAGCATATCAG
CCTTATCTTGGTTGATCGGCATGCTGGACGAGCACATCTGTTGTCGCATCAACTGCTGACTGCTATATATGTGCTG
GTGCTGAATCGATCGATTGTCGTCGCGGAAGTGAAGAACAACCACGGCACTGCTGCCTGCTGGGCTCTAGCCGCCA
TCAGTTATAACCGTACAAACTTCAGTGATTTGCTGGTTTCACATTGGTTTATAATAAAGGCCTCCGTTTTTAGTTT
CACGCTGGGCCTTCAGAATCTCAGGACCGGCCCTGCTCATGATCCTTACACCGTGTATCCTGTAGAGTACTTCTCT
AAAAGAGAGTACCCTAGTGGAAGTAGCAAAGTTGCACCATCTGCTTCATACGAAAGATATGCAGCAACTACTCGCT
TGCCTAATGGAGAACTGCCCTCATCTATTAGTCCTGGTGCCGATTATATGTCCTGCCGTTCTTATCTTGACCAAGT
ACCTACTGATAGGTACTCTAATAGGGTTACACTACAATTAGGCCTCTCGAGAGCCGGGAATAGTAATGTGCAACAA
TTAGGAATCACCAGAGCTGGAAATTCCAATGCTTATGATTATACTGAGGCTGCTGAGCAGATCCATGGACGTGAGG
ATTACCGAAGACTGTCAGGTCTCACTGGGTATCCAGGTGGCTCTTCGAATTGTGGATTCCAAATAGTTAACTGGAG
TCTGTCATTGGTGTTGGTGATCTCTGGTGCGAGAGTGAAGTTGCACGAAGCCCATCCTGGTTCTTCCGAGTCCATT
GTGGAGATCCAGGGCATTCCGGATCAAGTGAAAGCCGCACAGAGCCTTCTGCAAGGCTTCATCGGCGCAAGCAGCA
ACAGCAGGCAGGCGCCCCAGTCCTCTCGCATGGCCCATTATTTTTAG

Rhpr3 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0052] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 24 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 25 as follows:

MARRAASRAVGALRSDGSIQGRGGRAGGSGAEDARHVFDELLRRGRGASIYGLNRALADVARHSPAAAVSRYNRMA
RAGADEVTPDLCTYGILIGCCCRAGRLDLGFAALGNVIKKGFRVEAITFTPLLKGLCADKRTSDAMDIVLRRMTEL
GCIPNVFSYNNLLNGLCDENRSQEALELLHMMADDRGGGSPPDVVSYTTVINGFFKEGDSDKAYSTYHEMLDRGIL
PDVVTYSSIIAALCKGQAMDKPWSHCKEGRVIESEKLFDLMVRIGVKPDIITYSTLIDGYCLAGKMDEAMKLLSGM
VSVGLKPNTVTYSTLINGYCKISRMEDALVLFKEMESSGVSPDIITYNIILQGLFQTRRTAAAKELYVRITESGTQ
IELSTYNIILHGLCKNKLTDDALQMFQNLCLMDLKLEARTFNIMIDALLKVGRNDEAKDLFVAFSSNGLVPNYWTY
RLMAENIIGQGLLEELDQLFLSMEDNGCTVDSGMLNFIVRELLQRGVVVVVSGESATTPPPTLKILTCGITVNPFS
KTCGITVNPFSKPIVQTGACGQVKEVGKNASEERLIVVSSQEIPDDPVSPTIEALILLHSKASTLAENHQLTTRLV
VPSNKVGCILGEGGKVITEMRRRTGAEIRVYSKADKPKYLSFDEELVQHISLILVDRHAGRAHLLSHQLLTAIYVL
VLNRSIVVAEVKNNHGTAACWALAAISYNRTNFSDLLVSHWFIIKASVFSFTLGLQNLRTGPAHDPYTVYPVEYFS
KREYPSGSSKVAPSASYERYAATTRLPNGELPSSISPGADYMSCRSYLDQVPTDRYSNRVTLQLGLSRAGNSNVQQ
LGITRAGNSNAYDYTEAAEQIHGREDYRRLSGLTGYPGGSSNCGFQIVNWSLSLVLVISGARVKLHEAHPGSSESI
VEIQGIPDQVKAAQSLLQGFIGASSNSRQAPQSSRMAHYF

[0053] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr4*, which has a nucleotide sequence of SEQ ID NO: 26, as follows:

ATGCCGCTCGCCACGCTGCTCGGCCACCTCGCCGCCGGCCGCTTCGGCCTCGTGCAGGCGCTCACCGGCGCCGCGA
CCGCGGCGGCCGCGCACCGACTCCTCCACCTCCTCCTCCGCACAGCGCCGCCGCCTCCCCTCCCGGACCTCGTCTC
CCTCGCGCGGTGGTCGCGCGCCCACTTCCGCGCGCCGCTCCCGCTCCGGCTCCACGGGCTCCTCCTCGCCCGCCTC
GCCTCCAAGGGGCTCTACCCCCTCCTCCGCTCCGAGCTCCACGTCCTCGCCGCGGCGCGCCTCCACTCCCCCGCAT
CCATCCTCCGCGCTCTCCCCTCCCCGTCCGCGTCCGCGTCCGCATCCACGCCGCTCATCGCCGACATGCTCGTCCT
CGCCCTCGCCAGGGCATCCCAGCCCCTCAGGGCGTACGACGCGTTCCTCCTCGCCGGGGAGAGCCACCCGCGGCAC
CGCCCCTCCACCTCCTCCGTGAACGCCCTTCTCGCCGGCCTCGTCGGCGCCAAGCGGGTCGACCTCGCCGAGAAGG
CGTTCAGGAGCGCGCTGCGGCGGCGCGTGTCACCGGACATCTACACCTTCAACACCGTCATCTCCGGCCTCTGCAG
GATCGGCCAGCTCCGCAAAGCCGGCGATGTCGCCAAGGACATCAAGGCATGGGGTCTGGCTCCCTCTGTGGCCACC
TACAATAGCCTCATCGATGGGTACTGCAAGAAGGGTGGAGCTGGGAACATGTACCATGTCGACATGCTTTTGAAGG
AGATGGTCGAAGCCGGGATCTCACCGACTGCAGTTACATTTGGTGTGTTGATCAATGGGTATTGCAAGAACTCGAA
TACTGCGGCCGCAGTGAGAGTCTTCGAGGAGATGAAGCAGCAGGGGATCGCTGCGAGTGTCGTGACGTATAATTCG
CTAATTTCAGGTCTCTGCAGTGAGGGTAAGGTGGAGGAAGGGGTGAAGCTGATGGAGGAGATGGAGGATTTGGGGC
TGTCACCCAATGAAATCACCTTTGGCTGTGTTCTGAAAGGGTTTTGTAAGAAGGGAATGATGGCAGATGCCAATGA
TTGGATTGATGGTATGACAGAGAGGAATGTGGAACCTGATGTGGTTATTTACAATATCTTGATCGATGTGTATCGC
CGTCTTGGAAAAATGGAGGATGCAATGGCGGTGAAGGAGGCAATGGCAAAGAAGGGGATCAGTCCCAATGTCACAA
CATATAATTGCTTGATAACAGGGTTTAGCCGCAGTGGGGATTGGAGGAGTGCTTCTGGCCTTCTGGATGAGATGAA
GGAGAAAGGTATTGAAGCAGACGTCGTCACTTACAATGTGCTTATTGGTGCTTTGTGCTGCAAAGGTGAGGTACGG
AAAGCTGTAAAGCTCTTGGATGAAATGTCGGAAGTTGGATTGGAACCAAACCATCTGACCTACAATACCATAATAC
AGGGGTTCTGTGATAAGGGTAACATTAAGTCTGCCTATGAAATTAGAACCAGGATGGAAAAATGTCGGAAACGGGC
AAATGTGGTTACGTACAATGTGTTCATCAAGTATTTCTGCCAGATAGGGAAGATGGATGAAGCTAATGATCTACTC
AATGAGATGTTGGACAAATGTCTAGTTCCAAACGGGATCACTTATGAAACGATAAAAGAGGGGATGATGGAAAAAG
GCTATACACCAGATATTAGAGGGTGCACTGTCTCACAAGCTTCTGAAAACCCAGCATCATCCTGA

Rhpr4 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0054] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 26 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 27 as follows:

MPLATLLGHLAAGRFGLVQALTGAATAAAAHRLLHLLLRTAPPPPLPDLVSLARWSRAHFRAPLPLRLHGLLLARL
ASKGLYPLLRSELHVLAAARLHSPASILRALPSPSASASASTPLIADMLVLALARASQPLRAYDAFLLAGESHPRH
RPSTSSVNALLAGLVGAKRVDLAEKAFRSALRRRVSPDIYTFNTVISGLCRIGQLRKAGDVAKDIKAWGLAPSVAT
YNSLIDGYCKKGGAGNMYHVDMLLKEMVEAGISPTAVTFGVLINGYCKNSNTAAAVRVFEEMKQQGIAASVVTYNS
LISGLCSEGKVEEGVKLMEEMEDLGLSPNEITFGCVLKGFCKKGMMADANDWIDGMTERNVEPDVVIYNILIDVYR
RLGKMEDAMAVKEAMAKKGISPNVTTYNCLITGFSRSGDWRSASGLLDEMKEKGIEADVVTYNVLIGALCCKGEVR
KAVKLLDEMSEVGLEPNHLTYNTIIQGFCDKGNIKSAYEIRTRMEKCRKRANVVTYNVFIKYFCQIGKMDEANDLL
NEMLDKCLVPNGITYETIKEGMMEKGYTPDIRGCTVSQASENPASS

[0055] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr5*, which has a nucleotide sequence of SEQ ID NO: 28, as follows:

ATGGCTGATGATGGTCGCTGCCCACCTGATGTGGTGTCGTATAATACCATCATTGATGGTCTCTTCAAAGAGGGTG
ATGTGGACAAAGCTTACATCACATACCATGAAATGCTGGACCGGAGGGTTTCTCCAGATGCTGTGACTTACAACTC
TATCATTGCTGCCTTAAGCAAGGCTCAAGCTATGGACAGGGCCATGGAGGTACTTACAGTGATGGTTATGCCCAAT
TGCTTCACATATAATAGTATTATGCATGGATATTGTTCTTCAGGACAGTCGGAAAAGGCTATTGGTATTTTCAGAA
AGATGTGCAGTGATGGTATTGAACCAGATGTTGTTACTTATAACTCGTTGATGGACTATCTCTGCAAGAACGGAAA
ATGCACAGAAGCCAGAAAGATTTTTGATTCTATGGTCAAGAGGGGTCTCAAGCCTGATATTACTACCTATGGTACC
CTGCTTCATGGGTATGCTTCCAAAGGAGCTCTTGTTGAGATGCATGATCTCTTAGCTTTGATGGTACAAAATGGCA
TGCAACTTGATCATCATGTCTTCAACATATTAATATGTGCATACACTAAACAAGAAAAAGTAGACGAGGTCGTGCT
TGTATTCAGCAAAATGAGGCAGCAAGGATTGACTCCGAACGCAGTGAACTATAGAACAGTGATAGATGGACTTTGC
AAGTTAGGTAGACTAGATGATGCTATGCTTAATTTTGAGCAGATGATTGATAAAGGACTGACACCTAACGTTGTTG
TTTATACCTCCCTAATTCATGCTCTCTGTACCTATGACAAATGGGAGAAGGCCGAGGAGTTAATTTTTGAAATATT
GGATCAAGGTATCAATCCCAACATTGTGTTTTTTAATACAATATTGGACAGTCTTTGCAAAGAAGGGAGGGTTATA
GAATCTAAAAAACTCTTTGACCTGTTGGGACATATTGGTGTGAATCCTGATGTCATTACATACAGTACACTCATCG
ATGGATATTGCTTAGCTGGTAAGATGGATGGAGCAATGAAGTTACTCACTGGCATGGTCTCAGTTGGGTTGAAACC
TGATAGTGTTACATATAGCACTTTGATTAATGGTTACTGTAAAATTAATAGAATGGAGGACGCATTAGCTCTTTTC
AAGGAGATGGAAAGCAATGGTGTTAATCCTGATATTATTACATATAACATAATTCTGCATGGTTTATTTCGCACCA
GAAGAACTGCTGCTGCAAAAGAACTATATGCCAGGATTACCGAAAGTGGAACGCAGCTTGAACTTAGCACATACAA
CATAATCCTCATGGACTTTGCAAAAACAAACTCACTGATGATGCACTTCGGATGTTTCAGAACCTATGTTTGA

Rhpr5 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0056] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 28 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 29 as follows:

MADDGRCPPDVVSYNTIIDGLFKEGDVDKAYITYHEMLDRRVSPDAVTYNSIIAALSKAQAMDRAMEVLTVMVMPN
CFTYNSIMHGYCSSGQSEKAIGIFRKMCSDGIEPDVVTYNSLMDYLCKNGKCTEARKIFDSMVKRGLKPDITTYGT
LLHGYASKGALVEMHDLLALMVQNGMQLDHHVFNILICAYTKQEKVDEVVLVFSKMRQQGLTPNAVNYRTVIDGLC
KLGRLDDAMLNFEQMIDKGLTPNVVVYTSLIHALCTYDKWEKAEELIFEILDQGINPNIVFFNTILDSLCKEGRVI
ESKKLFDLLGHIGVNPDVITYSTLIDGYCLAGKMDGAMKLLTGMVSVGLKPDSVTYSTLINGYCKINRMEDALALF
KEMESNGVNPDIITYNIILHGLFRTRRTAAAKELYARITESGTQLELSTYNIILMDFAKTNSLMMHFGCFRTYV

[0057] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr6*, which has a nucleotide sequence of SEQ ID NO: 30, as follows:

ATGGCGCGCCGCGCCGCTTCCCGCGCTGTTGGCTCGGAGGGCTCGATCCAAGGGCGAGGGGGCCGCGCGGGGGGCA
ATGGCGCCGAGGACGCACGCCACGTGTTCGACGAATTGCTTCGGCGTGGCAAGGGCGCCACGATCTACGGCTTGAA
CCGCGCCCTCGACGACGTCGCGCGTCACAGCCCCGCGGCCGCCGTGTCCCGCTACAACCGCATGGCCCGAGCCGGC
GCCGACGAGGTAACTCCCAACTTGTACACCTACAGCGTTCTCATCGGTTGCTGCTGCCGGGCGGGCCGCTTGGACC
TCGGTTTCGCGGCCTTGGGCAATGTCATTAAGAAGGGATTTAGAGTGGAAGCCATCACCTTCACTCCTCTGCTCAA
GGGCCTCTGTGCCGACAAGAGGACGAGCGACGCAATGGACATAGTGCTCTGCAGAATGACCCAGCTCGGCTGCATA
CCAAATGTCTTCTCCTGCACCATTCTTCTCAAGGGTCTGTGTGATGAGAACAGAAGCCAAGAAGCTCTCGAGCTGC
TCCAAATGATGCCTGATGATGGAGGTGACTGCCCACCTGATGTGGTGTTGTACAACACCGTCATCAATGGCTTCTT
CAAAGAGGGGGATCCGGACAAAGCTTACGCTACATACCATGAAATGTTTGACCAGGGGATTTTGCCAGATGTTGTG
ACTTACAGCTCTATTATCGCTGCCTTATGCAAGGCTCAAGCTATGGACAAGGCCATGGAGGTACTTAACACCATGG
TTAAGAATGGTGTCATGCCTAATTGCAGGACATATAATAGTATTGTGCACGGATATTGCTCTTCAGGGCAGTTGAC
AGAGGCTATTGGATTTCTCAAAATGATGTGCAGTGATGGTGTCGAACCAGATGTTGTTACTTGTAACTTGCTGATG
GATTATCTTTGCAAGAACAGAAGATGCACGGAAGCTAGAAAGATTTTCAATTCTATGACCAAGTGTGGCCTAAAGC
CTGATATTACTACCTATTGTACCCTGCTTCAGGGGTATGCTACCAAAGGAGCCCTTGTTGAGATGCATGATCTCCT
GGATTTGATGGTATGGAACGGTATCCAACCTAATCATCATGTATTCAACATTCTAATATGTGCATACGCTAAACAA
GAAAAAGTAGATGAGGCGATGCTTGTATTCAGCAAAATGAGGCAGCAAGGATTGAGTCCGAATGCAGTGAACTACA
GAACAGTCATAGATGTACTCTGCAAGCTAGGCAGAGTATACGATGCAGTGCTTACCTTAAAGCAGATGATCAATGA
AGGACTAACCCCTGACATCATTGTATATACCCCCCTAATTCATGGTTTTTGTACCTGTGACAAATGGGAGAAGGCT
GAGGAGTTAATTTTTTAA

Rhpr6 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0058] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 30 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 31 as follows:

MARRAASRAVGSEGSIQGRGGRAGGNGAEDARHVFDELLRRGKGATIYGLNRALDDVARHSPAAAVSRYNRMARAG
ADEVTPNLYTYSVLIGCCCRAGRLDLGFAALGNVIKKGFRVEAITFTPLLKGLCADKRTSDAMDIVLCRMTQLGCI
PNVFSCTILLKGLCDENRSQEALELLQMMPDDGGDCPPDVVLYNTVINGFFKEGDPDKAYATYHEMFDQGILPDVV
TYSSIIAALCKAQAMDKAMEVLNTMVKNGVMPNCRTYNSIVHGYCSSGQLTEAIGFLKMMCSDGVEPDVVTCNLLM
DYLCKNRRCTEARKIFNSMTKCGLKPDITTYCTLLQGYATKGALVEMHDLLDLMVWNGIQPNHHVFNILICAYAKQ
EKVDEAMLVFSKMRQQGLSPNAVNYRTVIDVLCKLGRVYDAVLTLKQMINEGLTPDIIVYTPLIHGFCTCDKWEKA
EELIF

[0059] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr7*, which has a nucleotide sequence of SEQ ID NO: 32, as follows:

ATGGCACGCCGCGTCGCTGCCCGCGCCCGCGCCCGCGCCGGCGGCGTCCCGCGCTCGGAGGGTACGATCCAAGACC
GAGCACGCGTTGGGAGCGGTGGCGCCGAGGACGCACTCGACGTGTTCGACGAATTGCTCCGGCGAGGCATCGGCGC
TCCGATCCGCAGCTTGAACGGCGCTCTCGCCGACGTCGCGCGCGACAACCCCGCGGCCGCTGTGTCCCGCTTCAAC
CGCATGGCACGAGCTGGTGCCAGCATGGTAACTCCCACCGTGCACACCTATGGCATCCTCATCGGCTGCTGCTGCA
GTGCGGGCCGCTTAGACCTCGGTTTCGCGGCCTTGGGCCATGTCGTTAAGAAGGGATTCAGAGTGGAACCCATCAT
CTTTAATCCTCTGCTCAAGGGCCTCTGTGCAGACAAGAGGACGGACGACGCAATGGACATAGTGCTCCGTGGAATG
ACCGAGCTCAGCTGCGTGCCAAATGTCTTCTCCCACACCATTATTCTCAAGGGACTCTGTCATGAGAACAGAAGCC
AAGAAGCTCTCGAGCTGCTCCACATGATGGCTGATGATGGAGGAGGCTGCTTACCTAATGTTGTGTCATACAGCAC
CGTCATCGATGGCCTCTTGAAAGGAGGGGATCCGGACAAAGCCTACGCTACATACCGTGAAATGCTTGACCGGAGG
ATTTTGCCAAATGTTGTGATTTACAGCTCCATTATTGCTGCCCTATGCAAGGGTCAAGCAATGGACAAGGCCATGG
AGGTACACGATAGGATGGTTAAGAATGGAGTTACACCCAATTGCTTCACGTATACTAGTCTTGTGCATGGATTTTG
CTCTTCAGGGCAGTTGACAGAGGCTATTAAATTTCTAGAAAAGATGTGCAGCAATGGTGTTGAACCAAATGTTGTT
ACTTATAGCTCGTTTATGGACTATCTCTGCAAGAACGGAAGATGCACAGAAGCTAGAAAGATTTTTGATTCTATGG
TCAAGAGGGGCCTAAAGCCTGATATTACTACCTACAGTAGCTTACTTCATGGGTATGCTATCGAAGGAGCTCTTGT
TGAGATGCATGGTCTCTTTGATTTGATGGTACAAAGTGATATGCAACCCGATCATTATGTCTTCAACACACTAATA
TATGCATCCGCCAAGCAAGGAAAAGTAGATGAGGCCATGCTTGTATTTAGCAAAATGAGGCAGCAAGGATTGAAAC
CTAATTGTGTTACGTATAGCACTTTGATTAATGGCTACTGTAAAATTACTAGGATGGAGAATGCTTTAGCACTTTT
CCAAGAGATGGTGAGCAATGGTGTTAGTCCTAATTTTATCACATATAACATAATGCTGCAAGGTTTATTTCGTACA
GGAAGAACTGCTACTGCAAAAGAATTCTATGTACAGATTATCAAAAGTGGCAAAAAAGATCTTATAGAACAGGGGT
TGCTAGAAGAATTGGATGATCTATTTCTTTCAATGGAGGACAATGACTGTAGTACTGTGTCGACTCCTGCATGCTA
A

Rhpr7 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0060] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 32 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 33 as follows:

MARRVAARARARAGGVPRSEGTIQDRARVGSGGAEDALDVFDELLRRGIGAPIRSLNGALADVARDNPAAAVSRFN
RMARAGASMVTPTVHTYGILIGCCCSAGRLDLGFAALGHVVKKGFRVEPIIFNPLLKGLCADKRTDDAMDIVLRGM
TELSCVPNVFSHTIILKGLCHENRSQEALELLHMMADDGGGCLPNVVSYSTVIDGLLKGGDPDKAYATYREMLDRR
ILPNVVIYSSIIAALCKGQAMDKAMEVHDRMVKNGVTPNCFTYTSLVHGFCSSGQLTEAIKFLEKMCSNGVEPNVV
TYSSFMDYLCKNGRCTEARKIFDSMVKRGLKPDITTYSSLLHGYAIEGALVEMHGLFDLMVQSDMQPDHYVFNTLI
YASAKQGKVDEAMLVFSKMRQQGLKPNCVTYSTLINGYCKITRMENALALFQEMVSNGVSPNFITYNIMLQGLFRT
GRTATAKEFYVQIIKSGKKDLIEQGLLEELDDLFLSMEDNDCSTVSTPAC

[0061] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr8*, which has a nucleotide sequence of SEQ ID NO: 34, as follows:

ATGGCGCGCCGCGCCGCTTCCCGCGCTGCTGGCGCCCTTCGCTCGGAGGGCTCGATCCAAGGGCGAGGGGGCCGCG
CGGGGGGCAGTGGCGGTGGCGCGGAGGACGCACGCCACGTGTTCGACGAATTGCTCCGTCGTGGCATACCAGATGT
CTTCTCCTACAATATTCTTCTCAACGGGCTGTGTGATGAGAACAGAAGCCAAGAAGCTCTCGAGTTACTGCACATA
ATGGCTGATGATGGAGGTGACTGCCCACCTGATGTGGTGTCGTACAGCACCGTCATCAATGGCTTCTTCAAGGAGG
GGGATCTGGACAAAATGCTTGACCAGAGGATTTCGCCAAATGTTGTGACCTACAACTCTATTATTGCTGCGCTATG
CAAGGCTCAAACTGTGGACAAGGCCATGGAGGTACTTACCACCATGGTTAAGAGTGGTGTCATGCCTGATTGCATG
ACATATAATAGTATTGTGCATGGGTTTTGCTCTTCAGGGCAGCCGAAAGAGGCTATTGTATTTCTCAAAAAGATGC
GCAGTGATGGTGTCGAACCAGATGTTGTTACTTATAACTCGCTCATGGATTATCTTTGCAAGAACGGAAGATGCAC
GGAAGCAAGAAAGATTTTTGATTCTATGACCAAGAGGGGCCTAAAGCCTGATATTACTACCTATGGTACCCTGCTT
CAGGGGTATGCTACCAAAGGAGCCCTTGTTGAGATGCATGGTCTCTTGGATTTGATGGTACGAAACGGTATCCACC
CTAATCATTATGTTTTCAGCATTCTAGTATGTGCATACGCTAAACAAGAGAAAGTAGAAGAGGCAATGCTTGTATT
CAGCAAAATGAGGCAGCAAGGATTGAATCCGAATGCAGTGACCTATGGAACAGTTATAGATGTACTTTGCAAGTCA
GGTAGAGTAGAAGATGCTATGCTTTATTTTGAGCAGATGATCGATGAAGGACTAAGACCTGACAGCATTGTTTATA
ACTCCCTAATTCATAGTCTCTGTATCTTTGACAAATGGGAGAAGGCTGAAGAGTTATTTCTTGAAATGTTGGATCG
AGGCATCTGTCTTAGCACTATTTTCTTTAATTCAATAATTGACAGTCATTGCAAAGAAGGGAGGGTTATAGAATCT
GGAAAACTCTTTGACTTGATGGTACGAATTGGTGTGAAGCCCGATATCATTACCCTTGGCAGGTTTTTGGGGAGCG
CAAGGCGCGACTACTCACTGTTCGTCAACATCTACTTCATCTTCACCAACATGTCGAACACTGGAGACAAGGAGAA
GGAGACTCCCGTCAACACCAACGGAGGCAATACTGCCTCAAACTCCAGCGGAGGACCATTCTTGGGCACATACAAC
ATAATCCTTCATGGACTTTGCAAAAACAAACTCACTGATGATGCACTTCGAATGTTTCAGAACCTATGTTTGATGG
ATTTGAAGCTTGAGGCTAGGACTTTCAACATTATGATTGATGCATTGCTTAAAGTTGGCAGAAATGATGAAGCCAA
GGATTTGTTTGTTGCTTTCTCGTCTAACGGTTTAGTGCCGAATTATTGGACGTACAGATTGATGGCTGAAAATATT
ATAGGACAGGGGTTGCTAGAAGAATTGGATCAACTCTTTCTTTCAATGGAGGACAATGGCTGTACTGTTGACTCTG
GCATGCTAAATTTCATTGTTAGGGAACTGTTGCAGAGAGGTGAGATAACCAGGGCTGGCACTTACCTTTCCATGAT
TGATGAGAAGCACTTTTCCCTCGAAGCATCCACTGCTTCCTTGTTTATAGATCTTTTGTCTGGGGGAAAATATCAA
GAATATCATATATTTCTCCCTGAAAAATACAAGTCCTTTATAGAATCTTTGAGCTGCTGA

Rhpr8 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0062] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 34 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 35 as follows:

MARRAASRAAGALRSEGSIQGRGGRAGGSGGGAEDARHVFDELLRRGIPDVFSYNILLNGLCDENRSQEALELLHI
MADDGGDCPPDVVSYSTVINGFFKEGDLDKMLDQRISPNVVTYNSIIAALCKAQTVDKAMEVLTTMVKSGVMPDCM
TYNSIVHGFCSSGQPKEAIVFLKKMRSDGVEPDVVTYNSLMDYLCKNGRCTEARKIFDSMTKRGLKPDITTYGTLL
QGYATKGALVEMHGLLDLMVRNGIHPNHYVFSILVCAYAKQEKVEEAMLVFSKMRQQGLNPNAVTYGTVIDVLCKS
GRVEDAMLYFEQMIDEGLRPDSIVYNSLIHSLCIFDKWEKAEELFLEMLDRGICLSTIFFNSIIDSHCKEGRVIES
GKLFDLMVRIGVKPDIITLGRFLGSARRDYSLFVNIYFIFTNMSNTGDKEKETPVNTNGGNTASNSSGGPFLGTYN
IILHGLCKNKLTDDALRMFQNLCLMDLKLEARTFNIMIDALLKVGRNDEAKDLFVAFSSNGLVPNYWTYRLMAENI
IGQGLLEELDQLFLSMEDNGCTVDSGMLNFIVRELLQRGEITRAGTYLSMIDEKHFSLEASTASLFIDLLSGGKYQ
EYHIFLPEKYKSFIESLSC

[0063] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr9*, which has a nucleotide sequence of SEQ ID NO: 36, as follows:

ATGGCGAGAAGAGGACGACGATACTGTAGAGCAGAGGGAACAGAGGAGCGGGGCACTGGTGCTCCGGTGGCTGGGA
GGTGGCGACGTCGGCGGCCGAATGTGTTCCCGAGCGCCGCGCTGGAGAGCCCCGAGCTGCGACGGCATCACGCCGA
CTACCGGCCGTGGGCGGCGCACATGGAGGCAAAGCCGGTCTACTTCGCGTCGAGGCGTGCCTCCGGGCGGCCCGAG
CTGCAGCAGCAGCTCGTCCGGCCCACCCCAATCTGGGCCGATTGGGCCGATCTCAGCCTCCCGGAGCGGAGACCGA
TCTGGGCCGTCCATCCGCGCCGCCCAGCCAATCGGACGGTGGGTGTATTACTGTACTGCCAGGTCGGTGACCCTCC
GCCGCCGGCGGCGGCGGCGGCGGCGGCAGGCATGGCGCGCCGTGTCACCACCCTTACCCGCGCCCGCACCCGCGCC
CGCGGCGGCGGCGTCCCCAGCGCGCAGGGTGGTACGACCCAAGACCTAGGGCGCGCGGGGGGCAGTGGCACCGAGG
GCGCACGCCACGTGCTCGACGAATTGCCGCTACGGGGCTGGGGCGCCTCGATCTACAGCTTCAACCGCACCCTCAC
CGACGTCGCGCGTGACAGCCCAGCCGCAGCAGTTTCGCTCTTCAACCGCATGGCCCGAGCCGGCGCCGACGAGGTA
ACTCCCGACTTGTGCACCTACAGCATTCTCATCGGTTGCTGCTGCCGCGCGGGCCGCTTGGACCTCGGTTTCGCGG
CCTTGGGCAATGTCATTAAGAAGGGATTTAGAGTGGAAGCCATCACCTTCGCTCCTCTGCTCAAGGGCCTCTGTGC
CGACAAGAGGACGAGCGACGCAATGGACATAGTGCTCCGCAGAATGACCGAGCTCAGCTGCATGCCAGATGTTTTC
TCCTGCACCATTCTTCTCAAGGGTCTGTGTGATGAGAACAGAAGCCAAGAAGCTCTCGAGCTGCTGCACATGATGG
CTGATGATCGAGGAGGAGGTAGCCCACCTGATGTGGTGTCGTATACCACTGTCATCAATGGCTTCTTCAAAGAGGG
GGATTCAGACAAAGCTTACAGTACATACCATGAAATGCTTGATCGGAGGATTTCACCAAATGTTGTGACCTACAGC
TCTATTATTGCTGCGTTATGCAAGGCTCAAGCTATGGACAAAGCCATGGAGGTACTTAACACCATGGTTAAGAATG
GTGTCATGCCTGATTGCATGACATATAATAGTATTCTGCATGGATATTGCTCTTCAGGGCAGCCAAAAGAGGCTAT
TGGAACACTCAAAAAGATGCGCAGTGATGGCGTCGAACCAAATGTTGTTACTTATAGATCACTGATGAATTATCTT
TGCAAGAATGGAAGATGCACCGAAGCTAGAAAGATTTTCGATTCTATGACCAAGAGGGGCCTAGAGCCTGATATTG
CTACCTATCGTACCCTGCTTCAGGGGTATGCTACCAAAGGAGCCCTTGTTGAGATGCATGCTCTCTTGGATTTGAT
GGATCCTGAGTTCTACAAGTATTTGGAGAAGTGA

Rhpr9 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0064] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 36 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 37 as follows:

MARRGRRYCRAEGTEERGTGAPVAGRWRRRRPNVFPSAALESPELRRHHADYRPWAAHMEAKPVYFASRRASGRPE
LQQQLVRPTPIWADWADLSLPERRPIWAVHPRRPANRTVGVLLYCQVGDPPPPAAAAAAAGMARRVTTLTRARTRA
RGGGVPSAQGGTTQDLGRAGGSGTEGARHVLDELPLRGWGASIYSFNRTLTDVARDSPAAAVSLFNRMARAGADEV
TPDLCTYSILIGCCCRAGRLDLGFAALGNVIKKGFRVEAITFAPLLKGLCADKRTSDAMDIVLRRMTELSCMPDVF
SCTILLKGLCDENRSQEALELLHMMADDRGGGSPPDVVSYTTVINGFFKEGDSDKAYSTYHEMLDRRISPNVVTYS
SIIAALCKAQAMDKAMEVLNTMVKNGVMPDCMTYNSILHGYCSSGQPKEAIGTLKKMRSDGVEPNVVTYRSLMNYL
CKNGRCTEARKIFDSMTKRGLEPDIATYRTLLQGYATKGALVEMHALLDLMDPEFYKYLEK

[0065] Another suitable nucleic acid molecule in accordance with the present invention is isolated from rice and identified herein as *Rhpr10*, which has a nucleotide sequence of SEQ ID NO: 38, as follows:

ATGCCCTTCCGACCGCGCCTCCCGCTCCCCCTCCTCCTCCTCCTCCTGCCTCACCTCCGGCGCCGCCGCTCCTCCC
CCCGCCCGCCCGTGCCCGCGTGGAGACCGCTCTCGTATTATCCCTCGGCGGCGGCCGCGGCGGCGGAGGTGACGGA
GTCCGAGGAGGACGCGGCGGCTGTTGGCAGGGACACCCGAGCCCCTCCCTCCATCGGCGGGATTGCACGGGGAGCG
CCTAGGGTTGGCTGCAATGGCGGGGGGGCTGCCGATGACGAGGAGGTCGAGAGGAAGGCCCGCGCTGTCGCGCGGA
TCAAGCTCTGCCATGAGCTTCTGCGGGAGAGGAGGTGGCGCGCGATGCGGGCAGCCTTGGCGCAGCTGGTGACTGA
GCAAGGTGAGCATGCTATGAATTTTCCCCATTCTGATTATCAACTCTACTCATGTGGTATCTGAATAACTATGGTG
ATTGGTGTGAGGAGGCGTAGGAATGGCATCGGTAGTTTTGAACTTCTGATCGATATGAATGTGTGACACAGGATAT
ATTGTTTTTCCAGAGGCATTATCAATTGATCATTACCATATAAAAAACAGTAAGAAAAGGGTCGAAAGCAATGCAT
ACATAGTTGTATTTGGTGTAGTATTATTACTGTAATTCGTTTTTTACTAGAAGGTCTCTGCAAGTATGACAAACTA
GTAACATAAAAATTGTTCGCGTTTAATCTTATTGCGCTTCCTGCTGTAGGATCTGGGTCTGCAGCTGCTCTCTGTG
ACATCTTATGGAACAGATTCAGAGAGTGTGATTCCAACGGTTGTGTATGGGATGCTCTAGCGAACAGTTATGCTAG
AGCTCAGATGGTTCATGATGCCCTTTACGTTCTTAGTAAAATGAGCAGCCTAAACATGCAAATCTCGGTGTTCACC
TATGACAGTTTATTGCACGGCTTAAGGATGACAGACGTGGCATTGGAGCTTTTTGAAGAAATGGAGTCTTGTGGTG
TCTCTCCCAGTGAATATTCGCATAGTATTATTATTAATGGCCTCTGTAAGCAAGATAAGGTTGGAGAAGCTTTATC
TTTCCTTCAGGAAGCTAGGAAGGAGGGAAAGTTTAAACCCTTGGGAATGACCTTTAACATTCTTATGTCTGCATTG
TGTAATTGGGGGTTTGTTCAGTCTGCAAAATCATTTTTATGCCTGATGCTGAAATATGGATTAGTCCCTGACAGGT
ATACCTTTTCTACCCTTATACACGGTCTATGTAAAGTAGGTTCAATGGAGGAAGCATTGGATCTTTTCGAGAGAGT
GACAAAAGAAGGAATGGAACTTGAGATTGTGACCTACAATAGCCTTATCAATGGGTACCGATTGCTTGGTTTAACA
AAAGAAATTCCTAAAATCATCCAGATGATGAGAGGCCAAGGTGTTGAACCTGATCTTGTTACATATACTATACTTA
TTGCTGGTCACTGCGAAAGTGGTGATGTTGAAGAAGGAATGAAGGTAAGGAAGGATGTCCTAGACCAAGGTTTGCA
GTTGAATATTGTCACATATAGTGTCCTTCTCAATGCTCTCTTCAAAAAAGGCATGTTCTGCGAAATTGACAACCTA
CTCGGCGAGATCTACAATATTGGTTTGGATATGGATGTTATCGCATATTCCATCCTTATCCATGGGTATTGCAAGC
TAGGGGAAATTGAAAAGGCTCTTCAAGTATGTAATGCAATGTGCAGTTCTCAGAGGGTAATGCCAACATCACTGAA
CCATTTTTCTATTCTTCTAGGACTTTGCAAGAAAGGATTGTTAGTTGAAGCAAGGTGGTATTTGGAAAATGTAGCT
AGAAAATATCAGCCAACTGATGTAGTGTTCTATAATGTCGTTATTGATGGTTATGCAAAACTTGGTGATATTGTAA

ATGCTGTTCGTTTGTATGATCAGATCACTGTAGCTGGTATGCACCCAACCATTGTCACATGCAATTCTCTTCTATA
TGGGTATTGTAAAATTGGGGATCTGCAACTTGCCGAGAGCTATTTTAGGGCTATTCAGCTAAGTGGACTTCTACCA
ACAGCAGTGACATACACTACCTTGATGGATGCACTCTCTGAAGCTGGAGAAGTTAATACCATGCTAAGTCTTTTTG
ATGAAATGGTTGCAAAGAGGATCAAGGCAAATGCAGTAACTTACAGTGTCATTGTTAAAGGGCTTTGTAAGCAGCT
CAGATTTGATGAGGCTATCAATGTTCTCAAAGATATGGATAGCAAAGGTATTAATGCTGACCCGATAACTTACAAT
ACCCTTATACAAGGTTTCTGTGAATCAGAAAACGTTCAGATGGCTTTCCACATACATGACATCATGTTATGCCGTG
GCCTTGTGCCGACACCTGTTACTTATAACTTGCTTATTAATGTGCTGTGTTTGAAGGGAAAAGTTATTCAAGCAGA
AATACTTTTGGAGTCCCTCAGAGAAAATGGCATTAAGTTGAGAAAATTTGCGTACACAACACTTATCAAAGCTCAG
TGCGCAAAAGGAATGCCTATCAATGCTGTTTTGTTAGTTGGTAAGCTTCTAGATGCAGGATTTGAAGCTTCTATTG
AAGATTTCAGTGCAGCAATCAATCGACTTTGCAAAAGACAATTTGCCAAAGAAGCCTTTATGTTTGTCCCGATTAT
GCTATCTGTTGGTATTTACCCAGATACTCAAATATATTGTGTGCTAGGCAGAGCTCTGCAGAAAAATAGTGAGCTT
GTCTATCTACCCATATTAAATGCACTTGCTGTTAAAACTGGTATTTAA

Rhpr10 is a rice homolog of the *Petunia Rf-PPR592* gene.

[0066] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 38 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 39 as follows:

MPFRPRLPLPLLLLLLPHLRRRRSSPRPPVPAWRPLSYYPSAAAAAAEVTESEEDAAAVGRDTRAPPSIGGIARGA
PRVGCNGGGAADDEEVERKARAVARIKLCHELLRERRWRAMRAALAQLVTEQGSGSAAALCDILWNRFRECDSNGC
VWDALANSYARAQMVHDALYVLSKMSSLNMQISVFTYDSLLHGLRMTDVALELFEEMESCGVSPSEYSHSIIINGL
CKQDKVGEALSFLQEARKEGKFKPLGMTFNILMSALCNWGFVQSAKSFLCLMLKYGLVPDRYTFSTLIHGLCKVGS
MEEALDLFERVTKEGMELEIVTYNSLINGYRLLGLTKEIPKIIQMMRGQGVEPDLVTYTILIAGHCESGDVEEGMK
VRKDVLDQGLQLNIVTYSVLLNALFKKGMFCEIDNLLGEIYNIGLDMDVIAYSILIHGYCKLGEIEKALQVCNAMC
SSQRVMPTSLNHFSILLGLCKKGLLVEARWYLENVARKYQPTDVVFYNVVIDGYAKLGDIVNAVRLYDQITVAGMH
PTIVTCNSLLYGYCKIGDLQLAESYFRAIQLSGLLPTAVTYTTLMDALSEAGEVNTMLSLFDEMVAKRIKANAVTY
SVIVKGLCKQLRFDEAINVLKDMDSKGINADPITYNTLIQGFCESENVQMAFHIHDIMLCRGLVPTPVTYNLLINV
LCLKGKVIQAEILLESLRENGIKLRKFAYTTLIKAQCAKGMPINAVLLVGKLLDAGFEASIEDFSAAINRLCKRQF
AKEAFMFVPIMLSVGIYPDTQIYCVLGRALQKNSELVYLPILNALAVKTGI

[0067] Another suitable nucleic acid molecule in accordance with the present invention is isolated from *Arabidopsis thaliana*, which has a nucleotide sequence of SEQ ID NO: 40, as follows:

ATGAAGGCTTTGAGATTGATTCAGCCTCATCTCTTGAAGACAGGTAGTCTTAGAACTGATTTGCTCTGTACCATTT
CGAGTTTCTTTTCTAGCTGCGAACGAGACTTTTCAAGTATTAGCAATGGGAATGTCTGTTTCAGAGAGAGATTGAG
AAGTGGTATTGTTGATATTAAGAAAGATGATGCTATTGCTCTGTTCCAAGAAATGATTAGGTCTCGTCCTCTTCCT
AGTCTTGTTGATTTCAGTAGATTCTTTAGTGCCATTGCCAGAACAAAACAGTTCAATCTCGTGTTAGATTTCTGCA
AGCAACTGGAATTGAATGGGATTGCTCATAACATCTACACTTTGAATATCATGATCAACTGCTTTTGCCGGTGTTG
TAAAACTTGTTTTGCTTATTCTGTTTTGGGAAAAGTAATGAAGCTTGGGTATGAGCCTGACACAACCACGTTTAAC

ACTCTGATCAAAGGACTCTTTCTTGAGGGTAAAGTGTCTGAAGCTGTGGTTTTAGTCGATAGGATGGTGGAAAACG
GATGTCAACCTGATGTGGTTACTTATAATTCGATTGTAAATGGGATATGTAGATCAGGAGATACTTCTTTGGCCTT
GGATTTGCTCAGAAAGATGGAAGAAAGAAATGTTAAGGCTGATGTGTTTACTTACAGTACAATCATTGATAGTCTT
TGTAGAGATGGTTGCATAGACGCTGCAATTAGCCTTTTCAAGGAAATGGAGACGAAAGGGATTAAATCTAGTGTTG
TTACGTATAATTCTCTTGTGAGAGGTCTTTGTAAAGCCGGTAAATGGAATGATGGGGCACTGTTGTTGAAGGATAT
GGTGAGTAGGGAAATCGTCCCTAATGTCATCACTTTCAATGTATTACTTGATGTTTTTGTCAAAGAAGGGAAGCTT
CAGGAGGCTAATGAATTGTACAAAGAGATGATCACAAGAGGTATATCACCTAATATTATTACTTATAATACCTTGA
TGGATGGGTATTGTATGCAGAACCGTCTTAGTGAGGCCAACAATATGTTGGATCTTATGGTTAGGAATAAGTGCAG
TCCTGATATCGTGACTTTTACAAGTCTCATCAAAGGATATTGTATGGTGAAAAGAGTTGACGATGGTATGAAGGTC
TTCCGCAATATTTCTAAGAGAGGCTTGGTTGCCAATGCAGTTACTTATAGCATTCTTGTCCAAGGGTTTTGTCAAT
CCGGGAAAATAAAGCTCGCAGAGGAACTTTTCCAAGAAATGGTTTCACACGGTGTTCTTCCTGATGTTATGACGTA
TGGTATTTTGCTTGATGGCTTGTGTGACAATGGGAAGCTTGAAAAGGCATTGGAAATTTTTGAGGATTTACAAAAG
AGTAAGATGGATCTTGGTATTGTTATGTATACAACCATCATCGAGGGGATGTGCAAGGGTGGAAAAGTGGAAGATG
CCTGGAATTTATTCTGTAGCCTACCTTGTAAAGGAGTGAAGCCTAATGTTATGACATACACCGTGATGATTTCAGG
ATTATGTAAGAAAGGGTCACTGTCTGAAGCAAACATCTTGCTTAGAAAAATGGAGGAAGATGGGAATGCGCCAAAT
GATTGTACATACAACACACTAATCCGGGCACATCTCCGAGATGGTGACTTAACTGCATCAGCTAAACTTATTGAAG
AAATGAAGAGTTGTGGGTTCTCAGCAGATGCTTCCAGTATTAAGATGGTTATCGATATGTTATTGAGTGGTGAATT
GGACAAAAGCTTTCTAGATATGCTTTCGTAA

SEQ ID NO: 40 is a *Arabidopsis* homolog of the *Petunia Rf-PPR592* gene.

[0068] The nucleic acid molecule of the present invention which has the nucleotide sequence of SEQ ID NO: 40 encodes a protein or polypeptide having a deduced amino acid sequence corresponding to SEQ ID NO: 41 as follows:

MKALRLIQPHLLKTGSLRTDLLCTISSFFSSCERDFSSISNGNVCFRERLRSGIVDIKKDDAIALFQEMIRSRPLP
SLVDFSRFFSAIARTKQFNLVLDFCKQLELNGIAHNIYTLNIMINCFCRCCKTCFAYSVLGKVMKLGYEPDTTTFN
TLIKGLFLEGKVSEAVVLVDRMVENGCQPDVVTYNSIVNGICRSGDTSLALDLLRKMEERNVKADVFTYSTIIDSL
CRDGCIDAAISLFKEMETKGIKSSVVTYNSLVRGLCKAGKWNDGALLLKDMVSREIVPNVITFNVLLDVFVKEGKL
QEANELYKEMITRGISPNIITYNTLMDGYCMQNRLSEANNMLDLMVRNKCSPDIVTFTSLIKGYCMVKRVDDGMKV
FRNISKRGLVANAVTYSILVQGFCQSGKIKLAEELFQEMVSHGVLPDVMTYGILLDGLCDNGKLEKALEIFEDLQK
SKMDLGIVMYTTIIEGMCKGGKVEDAWNLFCSLPCKGVKPNVMTYTVMISGLCKKGSLSEANILLRKMEEDGNAPN
DCTYNTLIRAHLRDGDLTASAKLIEEMKSCGFSADASSIKMVIDMLLSGELDKSFLDMLS

[0069] Another nucleic acid molecule in accordance with the present invention has a nucleotide sequence of SEQ ID NO: 42, identified herein as *Rf-PPR591*, as follows:

1 ATATATATATACAAACTGATTTTTTCTGTCTATTTGCACAGTGTTATTTTTACATACCCTTGAAAAAGGGTAGCTCCGCT
81 AATAATGTTATCTTTACAAAAAATAACAATACTTTTTTTACATAATATATACAAAACTCATTCTTATGTATTGTAAATAT
161 GATAAAAATATTGTTATTTTTTGTAATATAGCTATTAGGTAGTCATGTTGTGTAAATTTTCCTAAAAATATTTACCTGAG
241 TCGGCCATTTGGCTAAAAATATTTCATTTTATAGTCGCATATACTCCAAGCTTGTATATCCCAGAGCGACAGTATACTTC

321 AATGGTATACGATATCTTCTATTATACACCTTTTTAGTATTCGTATACCCCCAATAGTATACAAGTTTGACACCGCAATA
401 GTGTACCCCAATGTTGTGGTTGTGTGGCTACAAAATTTGAGTGATGGTAGTGTAATTTTTTAGTGTAAGCTGGGTAGTTT
481 TGAAAACATTCTTTTTGAAAATTGTAGTTCAAGTCATAGTACAAAAAACTGAAATATTTATATGTTTCTTGATTCTGGCT
561 GGTCTTCTAAAAATTTTGAAATGCTGGCTAGTTTTCATTTAGCGAGGGGCAAATAGGCTACATGGCCAAATTTTTACGTT
641 AAAAGATAAGTGTTGTCTGGGAAAGTATTCGAAAAGATTGTAGGGACAAGTGTTGCCTAGACAACACGTCAAATTATGTA
721 GAAAAATGCACGAAGAAATTCAAAAGCAAATATTGCTTAAGCAAGAGGCAGTCAAAGACAAGTGCTGCCTTAGGGAGTGA
801 GAAATGGGCATCACTATAAGATTGTATTTCCATCCGATATTTATTCATTATAAACTTAAGGAAAAGTGCAGGAAAAACCA
881 CTAGTTTTTAGCTATTTTTTGGAACTTTAATCATTATGGGCTGAACTTCAGACTTTGTGGGCCGAACTTCATACATTCGC
961 AAGTAAAAATTTAGCTCACAGGCCACTTTTACCACTAGTATTTGGTTTGAAGTCATTTTTTATTGGTTTTACATGAGAGA
1041 CCACTTTTTGGAACTTCAATCTTTGTGCGCTTGAACTTCATGCCTAAGTTATTAAGTTCAACTTCAATCCGTAAGGGCTG
1121 AATTTTTAGGCATAGATGCGTAAACTTCAACCTTGTGGACTGAAGTTGAACTTCGCCCCTTATGGTGGCCTGAAGTTGAA
1201 CTTCAATCCTTGTGGGCTGAACTTGTGTGAAGTTCAACCCACAAGGATTAAAGTTTCAAAAAATGACCTCTCAAGCAAAA
1281 TCTGTAAAAAAAAAGTGGTCTCTCATGCACTTTTACCCATTCGCAAAGTAGGCTGAAGTTCAGCCCACAATTATTCAAGTT
1361 CCAAAAAATTTCACAATATATACCTCCTTATCTCGGTTATGATCTTTTGTATGATTTAGCAAAATGGACGGGGAAAGTGC
1441 ACGAAAGACCACTTTTGCCATTGGTCTTTGGGTACAGGCCACTAATACCAAAATATTTAGTTTGTGGCTACTTTTGCTTA
1521 AAGAGTTGAACTTCAGTCCAGAGGCCGGATTGAAGTTCAGTCCTTAAAGATTGAACTTCGATCCAGTGCCATATGGACTG
1601 AAGTTCAGTCAAGTCCTTAAGATGGAACTTCAGTCCAGAGCCATATGGACTGAAGTTCAGTCAATTATCAGAACTTAAGT
1681 CAATATTTATTTAGTAAAGGCCCAAAAGTGGTTAGTATAAGACCAATAAAAATAGCGGCCTAAAACTAAATAACAGTGTT
1761 AAAAGTGGCTGATGGACGAAATTTCTACAAAATGGACTCGAGGTAGCAATTCAACTTCAACCTATGGTGTCATAGTTGTA
1841 CAATTCTTCCAATCACCCCTACTAAGTGAAGTGAAGCGAAGATGATGAGAATTTCAGTGCGTTACTGTCTCAATGGTAAT
1921 CCCTTTTTCTCATTCTTTGCTTATTCAATTGCACCCCGACATTATTCTACCAATACATGTTCCATTTCAGTTAAAGGGAA
2001 TTTTGGGGTTTCTAATGAATTTCAGAATGTTAAGTGTTTAGATGATGCTTTCAGTTTGTTCCGTCAAATGGTTAGAACTA
2081 AGCCTCTTCCTTCTGTTGCCTCTTTCTCTAAATTGTTGAAAGCTATGGTACATATGAAGCATTACTCTTCTGTTGTTTCT
2161 CTTTTTCGAGAAATCCACAAATTACGAATTCCTGTTCATGAATTCATCTTGAGCATTGTGGTTAACAGTTGTTGCCTTAT
2241 GCATCGTACCGATCTCGGATTTTCTGTATTAGCCATTCACTTCAAGAAAGGCATTCCATATAATGAAGTCACCTTTACTA
2321 CCTTAATAAGGGGACTTTTTGCTGAAAATAAGGTCAAAGATGCTGTTCATTTGTTCAAAAAGTTGGTGAGGGAGAATATA
2401 TGTGAGCCTAATGAAGTCATGTATGGAACGGTCATGAATGGGCTTTGCAAAAAGGGCCATACTCAAAAAGCTTTTGATTT
2481 GCTCCGGTTAATGGAACAAGGAAGCACTAAGCCCAATACACGCACTTACACCATTGTCATAGACGCCTTTTGCAAAGATG
2561 GGATGCTAGATGGTGCTACCAGCCTTTTGAATGAGATGAAACAAAAAAGCATTCCTCCCGACATTTTTACTTATAGCACT
2641 TTAATTGATGCTTTGTGTAAGTTAAGTCAGTGGGAAAATGTTAGGACTTTGTTCCTTGAGATGATACATCTTAATATTTA
2721 TCCAAATGTGTGCACCTTCAACTCCGTCATTGATGGACTATGCAAAGAGGGGAAAGTAGAAGACGCTGAGGAAATAATGA
2801 GATACATGATTGAAAAAGGTGTAGACCCTGATGTGATCACCTATAATATGATAATTGACGGATATGGCTTGCGTGGTCAA
2881 GTGGATAGAGCACGGGAAATTTTTGATTCCATGATCAATAAGAGCATTGAGCCCGATATTATTAGCTATAATATACTAAT
2961 AAATGGATATGCCAGGCAAAAGAAAATAGACGAGGCAATGCAAGTCTGCCGTGAAATTTCTCAAAAGGGATTGAAACCTA
3041 GTATTGTTACCTGCAATGTTCTCTTGCATGGTCTTTTTGAACTTGGAAGAACTAAATCTGCACAAAATTTCTTTGATGAG
3121 ATGCTATCTGCGGGGCACATCCCTGATTTATACACTCATTGTACTTTGCTTGGTGGTTATTTTAAGAATGGACTTGTTGA
3201 AGAGGCTATGTCACACTTCCATAAGTTGGAAAGAAGGAGAGAAGATACAAATATTCAAATTTACACGGCTGTCATTGATG
3281 GATTGTGCAAAAATGGTAAGCTCGACAAAGCTCATGCTACGTTTGAGAAGCTTCCCTTGATAGGCTTACATCCTGATGTG
3361 ATAACATACACTGCAATGATTAGTGGATATTGTCAAGAAGGGTTGTTAGATGAAGCTAAAGATATGCTAAGGAAAATGGA
3441 GGACAATGGTTGTTTGGCAGACAACCGAACATACAATGTTATTGTGCGGGGATTTCTCAGAAGCAATAAAGTTAGTGAAA
3521 TGAAGGCTTTTCTGGAGGAAATAGCTGGGAAGAGCTTCTCATTTGAGGCAGCTACTGTAGAGTTATTGATGGATATTATA
3601 GCAGAGGATCCATCCATAACACGCAAAATGCACTGGATTAAACTGCACATTGCATGAATATACAAGGAGATTAGCAGAAT
3681 AATCACAGGTCCGTCCCAGACAACCCCAAGGCTAAATCCCACAATCGAAACAAGGTAAACTATTAATACTTTAACTGCCA
3761 AAACTTCTTTAAGAACTATGCCAATTGAAACAGGTAATATATATATTTCCTTTATTTGGAACATTTCTCGATTTATGCGT
3841 GTCATCCTTGTGCAGAGGCCATGCTAATCTTCTCTCAATCGTTCCCAGGTTTGATTTGAATGATATTTTAGATTATATAC
3921 CCCACAGTTCTGCATTGAAATATGCACCCAAACAAATTAGTGCATCTGTCATAAAAGGGATTGCTCCTATTATACCATCA
4001 TTAAGAAAATCCTTGTGACAGTCGGATAAATGAGCAAATAGTACATGTTTGTTTATTTTTTATTCAATAAGAGTTTGACA

4081 TCTACGGGAAATTATAGTTATCTATGTGGTCGTACTTTTAAAGAAAAGTATTTTTGTGGTTATAGATTGACTGTTTTCCT
4161 CTGTCATTGATCGACTTTCTTTTATTCACATCAGAAGTAGGTATATGTGTACAATGCTTTTAACAACTGGTTTGCATGTG
4241 CTCTTTATGGTCGCATTTCATCAACGAAGTCTCTTTGTCGAGATGCAGCTTGACTTGTTAAGACAAGAACCTTTCGATTT
4321 GGAAATGTGATTATCCCATTCAAAGATACTTGACAGATGTCTCATGATGCTTATTTGACTCAGAAGAATATTCAGAAAAG
4401 GCATGTAGATGTGCAGCAAATGACAGAGTATGTGCAATGGGTGAGGAGGACAATTATACATTGTCCTCCATTGTTCAGTG
4481 GCAAATGGCAATACACCTATGGGATCTAAAGGACATGTTCTGCATGTAGCTAGAAGGGATGCAAGTTCACAGGGAACTAG
4561 GGATTTGGTAGACTATACCAGCCTTCATTTTATCAGTTAGTGAAATGAAAGAAACCATCAATGTAAAGGAAACTCTATGG
4641 TTGTACACCTTTTGAAGTTCCAAGTGTTAAACTAACCTCTGGTGTATATTAGTATATACGGTAGAATTCATTCAATTGCA
4721 CAAGTAGATGTATCTTTTTGCTTGGTTTTAGTTCATTAAGGCATAAATGTTCTACTTAGGTTTCATGCATTAAAATGAAC
4801 ATTCATTTGATCTATGATGATGGAGTCTTGGTCGTGCATATACATGCTTCAAAATTATTGTACAATGGGTTGTGTAGTCC
4881 AATATGTTAACATCATCCACGACATTATCTCTAATAGTTTGAGATTTTGTGATATTTATTCGTAAAATGCATGTTAAGAT
4961 TATTGTAATTTAGACTTCTAAAGTTTTCTTTTTAGTTTGGTGGACAACAAAGTAATAAATCTCAAACACATTGTTTGGTC
5041 TCTTATTCTTTGGAATAAAATATTGAGCTTTTTACAATGTGTACCCTTGGAATATAAAGTATTTACCTTACTATACCTAT
5121 TAAAAATTACATTACTCATGAAATTCAAAGTATCTATCACACTGCGTATTTTTTTTTATACTATAAGTCTATATTTACCT
5201 TAGGGCAAAAATTAGGCAAGTACTTACCCACATCGGGTGTATATACCCAATCAACAAAGGAATTTTTACACTCTATACCC
5281 ATGAAATTTAAAGTATTTACAAGTCATACCCATTAAAAATTACTCTACCCATAAAACTAAAAGTATTTACCCAACATACC
5361 CATTTTTTATTGTATACCTTTGTTTATAGGTGTATACCTTTAAGGCTGCATAAATTATGGTATAAAAGTCTGGAGGACCA
5441 TTTATTATTGTTTACCTTTTTATACCTTATAATATATAAGTCTGGAGGGGTAGAGTGAGTAAATATTTTAATGGGTAGGC
5521 CAGATAATATTTGAAAGTAGTGGATAGTGGCTGTAATTATTTTAGATTTCGTGGGTATTTTTGTAAGTGTCTAATCAACA
5601 AATGCACGTCATTTGTTTACAATACACTACTATCACTTAGCCATAATTAATTAATAGACATTCTCTCTTCATTACATCAC
5681 ATTACCATAGTTAATTGCTATGGTTAGGTATATATATCCGGTGTGAGTAAATTTTTTCATATAAATTATGGCAAGACGAG
5761 TAAATATGAAACTTACATGCAGAGGCAGATAAATATTTTGATTTTGATGAGTATTTTCGTAAAACAATGATTAAATTATC
5841 GCGCAAAACCCTTTCAGTTTGTTTTAATCGTGTACTTATTTGTTTGTTATCATTCCATAATGAAAATTACCTCATTAGTG
5921 CCACATTATCTTTCTATAATGTGGCTATTGTGTCAAGAATCATAATCGTGCCAACTTGCTACATTGTAAAAACAATGATT
6001 CTTTTGTGGCTATTTAGTCAAAAATAGTAACTCTGCTTTCCATTGTCTCCGGTCACCTCGGCCAACTCCGGCCCTACGTT
6081 CATCAAGTACTTATTTTCCATATTTATTCGTTATTTTGTTAATACTTACAATTTGTTTAATTAAATCATAGAATTAGCTG
6161 ATACACACATATATAGTGAAAAATGAGATAGTAACTGAAGCAGCTCAAGTTCAATTTTTAGGTGCAAAATTCTTCTATCA
6241 GTTATTATGTTTTGCTTTCAAATTAATAACATATTCATATAGCCGACCTCAACTAATTACGCATTGATGCATAGTTCATT
6321 GTACTAGGAAAAGTAAAATTTCATTTTTAAGTTAGTTTATTTGAGCAAGTTATATATATATACACAATGCATGTGCTTAT
6401 ATCCCTTTCCAATGCTAACTCTGACTTCATGAAAATTAAATTATAGGTGTTACTTTAGTGAGGGACGCGAATTAATATTA
6481 CATCACTGGTAGTGGCGGAGCCAGTATTTTTACTAAGGAGTATCAAAATATAAATAAGTAAATATACGAAATATTAAAAG
6561 GATAGTGAATCTTCCTTTTTAATGTACTTCATTTTAAAGTTAGTTTATTTGAGAAAGTTATATATATACAATGTATGAAC
6641 TGATATTCTTTGATAATGATGATGCCTATGTGGATAGTGAATCTTCCTTTTTAATGTTGATGAAAAATAAA

Rf-PPR591, isolated from *Petunia*, has an open reading frame ("ORF") of 1776 bp, extending between nucleotides 1882-3657, which is homologous to that of *Rf-PPR592*.

[0070] The nucleotide sequence of SEQ ID NO: 42 encodes a protein or polypeptide having a deduced amino acid sequence of SEQ ID NO: 43, as follows:

MMRISVRYCLNGNPFFSFFAYSIAPRHYSTNTCSISVKGNFGVSNEFQNVKCLDDAFSLFRQMVRTKPLPSVASFS
KLLKAMVHMKHYSSVVSLFREIHKLRIPVHEFILSIVVNSCCLMHRTDLGFSVLAIHFKKGIPYNEVTFTTLIRGL
FAENKVKDAVHLFKKLVRENICEPNEVMYGTVMNGLCKKGHTQKAFDLLRLMEQGSTKPNTRTYTIVIDAFCKDGM
LDGATSLLNEMKQKSIPPDIFTYSTLIDALCKLSQWENVRTLFLEMIHLNIYPNVCTFNSVIDGLCKEGKVEDAEE

IMRYMIEKGVDPDVITYNMIIDGYGLRGQVDRAREIFDSMINKSIEPDIISYNILINGYARQKKIDEAMQVCREIS
QKGLKPSIVTCNVLLHGLFELGRTKSAQNFFDEMLSAGHIPDLYTHCTLLGGYFKNGLVEEAMSHFHKLERRREDT
NIQIYTAVIDGLCKNGKLDKAHATFEKLPLIGLHPDVITYTAMISGYCQEGLLDEAKDMLRKMEDNGCLADNRTYN
VIVRGFLRSNKVSEMKAFLEEIAGKSFSFEAATVELLMDIIAEDPSITRKMHWIKLHIA

[0071] Yet another nucleic acid molecule in accordance with the present invention has a nucleotide sequence of SEQ ID NO: 44, identified herein as *rf-PPR592*, as follows:

ATGATGAGAATTGCAGTGCGTTACTGTCTCAATGGTAATCCCTTTTTCTCATTCTTTGCTTATTCAATTGCACCCC
GACATTATTCTACCAATACACGTTCCATTTCAGTTAAAGGGAATTTTGGGGTTTCTAATGAATTTGAGAATGTTAA
GTGTTTAGATGATGCTTTCAGTTTGTTCCGTCAAATGGTTAGAACTAAGCCTCTTCCTTCTGTTGTCTCTTTCTCT
AAATTGTTGAAAGCTTTGGTACATATGAAGCATTACTCTTCTGTTGTTTCTCTTTTTCGAGAAATCCACAAATTAC
GTATTCCTGTTCATGAATTCATCTTGAGCATTGTGGTTAACAGTTGTTGCCTTATGCATCGTACCGATCTCGGATT
TTCTGTATTAGCCATTCACTTCAAGAAAGGTATTCCATTTAATCAAGTTATCTTTAACACCTTACTAAGGGGACTC
TTTGCTGAAAATAAGGTTAAAGATGCTGTTCATTTGTTCAAAAAGTTGGTGAGGGAGAATATATGTGAGCCTAATG
AAGTCATGTATGGAACGGTCATGAATGGGCTTTGCAAAAAGGGCCATACTCAAAAAGCTTTTGATTTGCTCCGGTT
AATGGAACAAGGAAGTACTAAGCCCAATACATGTATCTATAGCATTGTTATCGATGCCTTTTGCAAAGATGGGATG
CTAGATGGTGCTACCAGCCTTTTGAATGAGATGAAACAAAAAAGCATTCCTCCCGACATTTTTACTTATAGCACTT
TAATTGATGCTTTGTGTAAGTTAAGTCAGTGGGAAAATGTTAGGACTTTGTTCCTTGAGATGATACATCTTAATAT
TTATCCAAATGTGTGCACCTTCAACTCCGTCATTGATGGACTATGCAAAGAGGGGAAAGTAGAAGACGCTGAGGAA
ATAATGAGATACATGATTGAAAAAGGTGTAGACCCTGATGTGATCACCTATAATATGATAATTGACGGATATGGCT
TGCGTGGTCAAGTGGATAGAGCACGGGAAATTTTTGATTCCATGATCAATAAGAGCATTGAGCCCAATATTATTAG
CTATAATATACTAATAAATGGATATGCCAGGCAAAAGAAAATAGACGAGGCAATGCAAGTCTGCCGTGAAATTTCT
CAAAAGGGATTGAAACCTAGTATTGTTACCTGCAATGTTCTCTTGCATGGTCTTTTTGAACTTGGAAGAACTAAAT
CTGCACAAAATTTCTTTGATGAGATGCTATCTGCGGGGCACATACCTGATTTATACACTCATTGTACTTTGCTTGG
TGGTTATTTTAAGAATGGACTTGTTGAAGAGGCTATGTCACACTTCCATAAGTTGGAAAGAAGGAGAGAAGATACA
AATATTCAAATTTACACGGCTGTCATTGATGGATTGTGCAAAAATGGTAAGCTCGACAAAGCTCATGCTACGTTTG
AGAAGCTTCCCTTGATAGGCTTACATCCTGATGTGATAACATACACTGCAATGATTAGTGGATATTGTCAAGAAGG
GTTGTTAGATGAAGCTAAAGATATGCTAAGGAAAATGGAGGACAATGGTTGTTTGGCAGACAACCGAACATACAAT
GTTATTGTGCGGGGATTTCTCAGAAGCAATAAAGTTAGTGAAATGAAGGCTTTTCTGGAGGAAATAGCTGGGAAGA
GCTTCTCATTTGAGGCAGCTACTGTAGAGTTATTGATGGATATTATAGCAGAGGATCCTTCTTTGCTTAACATGAT
TCCAGAATTTCACCGGGATAATAAGAAGTGA

rf-PPR592 is a gene homologous to *Rf-PPR592* and is isolated from a non-restoring *Petunia* line.

[0072] The nucleotide sequence of SEQ ID NO: 44 encodes a protein or polypeptide having a deduced amino acid sequence of SEQ ID NO: 45, as follows:

MMRIAVRYCLNGNPFFSFFAYSIAPRHYSTNTRSISVKGNFGVSNEFENVKCLDDAFSLFRQMVRTKPLPSVVSFS
KLLKALVHMKHYSSVVSLFREIHKLRIPVHEFILSIVVNSCCLMHRTDLGFSVLAIHFKKGIPFNQVIFNTLLRGL
FAENKVKDAVHLFKKLVRENICEPNEVMYGTVMNGLCKKGHTQKAFDLLRLMEQGSTKPNTCIYSIVIDAFCKDGM
LDGATSLLNEMKQKSIPPDIFTYSTLIDALCKLSQWENVRTLFLEMIHLNIYPNVCTFNSVIDGLCKEGKVEDAEE
IMRYMIEKGVDPDVITYNMIIDGYGLRGQVDRAREIFDSMINKSIEPNIISYNILINGYARQKKIDEAMQVCREIS
QKGLKPSIVTCNVLLHGLFELGRTKSAQNFFDEMLSAGHIPDLYTHCTLLGGYFKNGLVEEAMSHFHKLERRREDT
NIQIYTAVIDGLCKNGKLDKAHATFEKLPLIGLHPDVITYTAMISGYCQEGLLDEAKDMLRKMEDNGCLADNRTYN
VIVRGFLRSNKVSEMKAFLEEIAGKSFSFEAATVELLMDIIAEDPSLLNMIPEFHRDNKK

[0073] Also suitable in the present invention are other forms of the nucleic acid molecules shown above. An example of a nucleic acid suitable in the present invention is a nucleic acid molecule which hybridizes to a nucleotide sequence of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, or SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

[0074] For the purposes of defining the level of stringency, reference can conveniently be made to Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press, at 11.45 (1989) which is hereby incorporated by reference in its entirety. An example of low stringency conditions is 4-6X SSC/0.1-0.5% w/v SDS at 37°-45° C for 2-3 hours. Depending on the source and concentration of the nucleic acid involved in the hybridization, alternative conditions of stringency may be employed such as medium stringent conditions. Examples of medium stringent conditions include 1-4X SSC/0.25% w/v SDS at > 45° C for 2-3 hours. An example of high stringency conditions includes 0.1-1X SSC/0.1% w/v SDS at 60 C for 1-3 hours. The skilled artisan is aware of various parameters which may be altered during hybridization and washing and which will either maintain or change the stringency conditions. For example, another stringent hybridization condition is hybridization at 4X SSC at 65° C, followed by a washing in 0.1X SSC at 65° C for about one hour. Alternatively, an exemplary stringent hybridization condition is in 50% formamide, 4XSSC, at 42° C. Still another example of stringent conditions include hybridization at 62° C in 6X SSC, .05X BLOTTO, and washing at 2X SSC, 0.1% SDS at 62° C.

[0075] The isolated nucleic acid molecule of the present invention can be from petunia, *Arabidopsis thaliana*, or rice.

[0076] The present invention also relates to an isolated protein encoded by the isolated nucleic acid molecule of the present invention which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant.

[0077] The present invention also relates to an isolated expression system that contains the nucleic acid molecule of the present invention which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant. This involves incorporating the nucleic acid molecules of the present invention into host cells using conventional recombinant DNA technology. Generally, this involves inserting the nucleic acid molecule into an expression system to which the nucleic acid molecule is heterologous (i.e., not normally present). The heterologous nucleic acid molecule is inserted into the expression system which includes the necessary elements for the transcription and translation of the inserted protein coding sequences. In one embodiment, the isolated expression system of the present invention contains the nucleic acid molecule of the present invention in proper sense orientation.

[0078] The nucleic acid molecules of the present invention may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art. Suitable vectors include, but are not limited to, the following viral vectors such as lambda vector system gt11, gt WES.tB, Charon 4, and plasmid vectors such as pBR322, pBR325, pACYC177, pACYC1084, pUC8, pUC9, pUC18, pUC19, pLG339, pR290, pKC37, pKC101, SV 40, pBluescript II SK +/- or KS +/- (see "Stratagene Cloning Systems" Catalog (1993) from Stratagene, La Jolla, CA, which is hereby incorporated by reference in its entirety), pQE, pIH821, pGEX, pET series (see Studier et al., "Use of T7 RNA Polymerase to Direct Expression of Cloned Genes," Gene Expression Technology, vol. 185 (1990), which is hereby incorporated by reference in its entirety), and any derivatives thereof. Recombinant molecules can be introduced into cells via transformation, particularly transduction, conjugation, mobilization, or electroporation. The DNA sequences are cloned into the vector using standard cloning procedures in the art, as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor, NY,

Cold Spring Harbor Laboratory Press (1989); and Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y., (1989) which are hereby incorporated by reference in their entirety.

[0079] In preparing a DNA vector for expression, the various DNA sequences may normally be inserted or substituted into a bacterial plasmid. Any convenient plasmid may be employed, which will be characterized by having a bacterial replication system, a marker which allows for selection in a bacterium and generally one or more unique, conveniently located restriction sites. Numerous plasmids, referred to as transformation vectors, are available for plant transformation. The selection of a vector will depend on the preferred transformation technique and target species for transformation. A variety of vectors are available for stable transformation using Agrobacterium tumefaciens, a soilborne bacterium that causes crown gall. Crown gall are characterized by tumors or galls that develop on the lower stem and main roots of the infected plant. These tumors are due to the transfer and incorporation of part of the bacterium plasmid DNA into the plant chromosomal DNA. This transfer DNA (T-DNA) is expressed along with the normal genes of the plant cell. The plasmid DNA, pTi or Ti-DNA, for "tumor inducing plasmid," contains the vir genes necessary for movement of the T-DNA into the plant. The T-DNA carries genes that encode proteins involved in the biosynthesis of plant regulatory factors, and bacterial nutrients (opines). The T-DNA is delimited by two 25 bp imperfect direct repeat sequences called the "border sequences." By removing the oncogene and opine genes, and replacing them with a gene of interest, it is possible to transfer foreign DNA into the plant without the formation of tumors or the multiplication of Agrobacterium tumefaciens (Fraley et al., "Expression of Bacterial Genes in Plant Cells," Proc. Nat'l Acad. Sci., 80:4803-4807 (1983), which is hereby incorporated by reference in its entirety).

[0080] Further improvement of this technique led to the development of the binary vector system (Bevan, "Binary *Agrobacterium* Vectors for Plant Transformation," Nucleic Acids Res., 12:8711-8721 (1984), which is hereby incorporated by reference in its entirety). In this system, all the T-DNA sequences (including the borders) are removed from the pTi, and a second vector containing T-DNA is introduced into *Agrobacterium tumefaciens.* This second vector has the advantage of being replicable in *E. coli* as well as *A. tumefaciens*, and contains a

multiclonal site that facilitates the cloning of a transgene. An example of a commonly used vector is pBin19 (Frisch et al., "Complete Sequence of the Binary Vector Bin19," Plant Molec. Biol., 27:405-409 (1995), which is hereby incorporated by reference in its entirety). Any appropriate vectors now known or later described for genetic transformation are suitable for use with the present invention.

[0081] U.S. Patent No. 4,237,224 issued to Cohen and Boyer, which is hereby incorporated by reference in its entirety, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including prokaryotic organisms and eukaryotic cells grown in tissue culture.

[0082] Certain "control elements" or "regulatory sequences" are also incorporated into the vector-construct. These include non-translated regions of the vector, promoters, and 5' and 3' untranslated regions which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used.

[0083] A constitutive promoter is a promoter that directs expression of a gene throughout the development and life of an organism. Examples of some constitutive promoters that are widely used for inducing expression of transgenes include the nopoline synthase ("NOS") gene promoter, from *Agrobacterium tumefaciens* (U.S. Patent No. 5,034,322 issued to Rogers et al., which is hereby incorporated by reference in its entirety), the cauliflower mosaic virus ("CaMV") 35S and 19S promoters (U.S. Patent No. 5,352,605 issued to Fraley et al., which is hereby incorporated by reference in its entirety), those derived from any of the several actin genes, which are known to be expressed in most cells types (U.S. Patent No. 6,002,068 issued to Privalle et al., which is hereby incorporated by reference in its entirety), and the ubiquitin promoter ("ubi"), which is the promoter of a gene product known to accumulate in many cell types.

[0084] An inducible promoter is a promoter that is capable of directly or indirectly activating transcription of one or more DNA sequences or genes in response to an inducer. In the absence of an inducer, the DNA sequences or genes will not be

transcribed. The inducer can be a chemical agent, such as a metabolite, growth regulator, herbicide or phenolic compound, or a physiological stress directly imposed upon the plant such as cold, heat, salt, toxins, or through the action of a pathogen or disease agent such as a virus or fungus. A plant cell containing an inducible promoter may be exposed to an inducer by externally applying the inducer to the cell or plant such as by spraying, watering, heating, or by exposure to the operative pathogen. An example of an appropriate inducible promoter for use in the present invention is a glucocorticoid-inducible promoter (Schena et al., " A Steroid-Inducible Gene Expression System for Plant Cells," Proc. Natl. Acad. Sci., 88:10421-5 (1991), which is hereby incorporated by reference in its entirety). Expression of the transgene-encoded protein is induced in the transformed plants when the transgenic plants are brought into contact with nanomolar concentrations of a glucocorticoid, or by contact with dexamethasone, a glucocorticoid analog (Schena et al., " A Steroid-Inducible Gene Expression System for Plant Cells," Proc. Natl. Acad. Sci. USA, 88:10421-5 (1991); Aoyama et al., "A Glucocorticoid-Mediated Transcriptional Induction System in Transgenic Plants," Plant J., 11: 605-612 (1997), and McNellis et al., "Glucocorticoid-Inducible Expression of a Bacterial Avirulence Gene in Transgenic Arabidopsis Induces Hypersensitive Cell Death, Plant J., 14(2):247-57 (1998), which are hereby incorporated by reference in their entirety). In addition, inducible promoters include promoters that function in a tissue specific manner to regulate the gene of interest within selected tissues of the plant. Examples of such tissue specific promoters include seed, flower, or root specific promoters as are well known in the field (U.S. Patent No. 5,750,385 issued to Shewmaker et al., which is hereby incorporated by reference in its entirety). In the preferred embodiment of the present invention, a heterologous promoter is linked to the nucleic acid of the construct, where "heterologous promoter" is defined as a promoter to which the nucleic acid of the construct is not linked in nature.

[0085] The nucleic acid construct also includes an operable 3' regulatory region, selected from among those which are capable of providing correct transcription termination and polyadenylation of mRNA for expression in the host cell of choice, operably linked to a DNA molecule which encodes for a protein of choice. A number of 3' regulatory regions are known to be operable in plants. Exemplary 3' regulatory regions include, without limitation, the nopaline synthase ("nos") 3'

regulatory region (Fraley et al., "Expression of Bacterial Genes in Plant Cells," Proc. Nat'l Acad. Sci. USA, 80:4803-4807 (1983), which is hereby incorporated by reference in its entirety) and the cauliflower mosaic virus ("CaMV") 3' regulatory region (Odell et al., "Identification of DNA Sequences Required for Activity of the Cauliflower Mosaic Virus 35S Promoter," Nature, 313(6005):810-812 (1985), which is hereby incorporated by reference in its entirety). Virtually any 3' regulatory region known to be operable in plants would suffice for proper expression of the coding sequence of the nucleic acid of the present invention.

[0086] The vector of choice, suitable promoter, and an appropriate 3' regulatory region can be ligated together to produce the nucleic acid construct which contains the nucleic acid molecule of the present invention, or suitable fragments thereof, using well known molecular cloning techniques as described in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press (1989); Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y. (1989), which are hereby incorporated by reference in their entirety.

[0087] Once the nucleic acid construct has been prepared, it is ready to be incorporated into a host cell. Accordingly, in another embodiment, the present invention is an isolated host cell containing the nucleic acid molecule of the present invention which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant. Basically, this method is carried out by transforming a host cell with the expression system of the present invention under conditions effective to yield transcription of the nucleic acid molecule in the host cell, using standard cloning procedures known in the art, such as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press, (1989), which is hereby incorporated by reference in its entirety. Suitable host cells include, but are not limited to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like. Preferably the host cells are either a bacterial cell or a plant cell. Methods of transformation may result in transient or stable expression of the DNA under control of the promoter. Preferably, the nucleic acid construct of the present invention is stably inserted into the genome of the recombinant plant cell as a result of the transformation, although transient expression can serve an important purpose,

particularly when the plant under investigation is slow-growing. Plant tissue suitable for transformation include leaf tissue, root tissue, meristems, zygotic and somatic embryos, callus, protoplasts, tassels, pollen, embryos, anthers, and the like. The means of transformation chosen is that most suited to the tissue to be transformed.

[0088] An appropriate method of stably introducing the nucleic acid construct into plant cells is to infect a plant cell with Agrobacterium tumefaciens or Agrobacterium rhizogenes previously transformed with the nucleic acid construct. As described above, the Ti (or RI) plasmid of Agrobacterium enables the highly successful transfer of a foreign DNA into plant cells. Another approach to transforming plant cells with a gene which imparts resistance to pathogens is particle bombardment (also known as biolistic transformation) of the host cell, as disclosed in U.S. Patent Nos. 4,945,050, 5,036,006, and 5,100,792, all to Sanford et al., and in Emerschad et al., "Somatic Embryogenesis and Plant Development from Immature Zygotic Embryos of Seedless Grapes (Vitis vinifera)," Plant Cell Reports, 14:6-12 (1995), which are hereby incorporated by reference in their entirety. Yet another method of introduction is fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies (Fraley et al., Proc. Natl. Acad. Sci. USA, 79:1859-63 (1982), which is hereby incorporated by reference in its entirety). The DNA molecule may also be introduced into the plant cells by electroporation (Fromm et al., Proc. Natl. Acad. Sci. USA, 82:5824 (1985), which is hereby incorporated by reference in its entirety). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the expression cassette. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and regenerate. The precise method of transformation is not critical to the practice of the present invention. Any method that results in efficient transformation of the host cell of choice is appropriate for practicing the present invention.

[0089] After transformation, the transformed plant cells must be regenerated. Plant regeneration from cultured protoplasts is described in Evans et al., Handbook of Plant Cell Cultures, Vol. 1, MacMillan Publishing Co., NY (1983); Vasil (ed.), Cell Culture and Somatic Cell Genetics of Plants, Acad. Press, Orlando, Vol. I, 1984, and Vol. III (1986); and Fitch et al., "Somatic Embryogenesis and Plant Regeneration

from Immature Zygotic Embryos of Papaya (Carica papaya L.)," Plant Cell Rep., 9:320 (1990), which are hereby incorporated by reference in their entirety.

[0090] Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

[0091] Preferably, transformed cells are first identified using a selection marker simultaneously introduced into the host cells along with the nucleic acid construct of the present invention. Suitable selection markers include, without limitation, markers encoding for antibiotic resistance, such as the nptII gene which confers kanamycin resistance (Fraley et al., "Expression of Bacterial Genes in Plant Cells," Proc. Natl. Acad. Sci. USA, 80:4803-4807 (1983), which is hereby incorporated by reference in its entirety), and the genes which confer resistance to gentamycin, G418, hygromycin, streptomycin, spectinomycin, tetracycline, chloramphenicol, and the like. Cells or tissues are grown on a selection medium containing the appropriate antibiotic, whereby generally only those transformants expressing the antibiotic resistance marker continue to grow. Other types of markers are also suitable for inclusion in the expression cassette of the present invention. For example, a gene encoding for herbicide tolerance, such as tolerance to sulfonylurea is useful, or the dhfr gene, which confers resistance to methotrexate (Bourouis et al., EMBO J., 2:1099-1104 (1983), which is hereby incorporated by reference in its entirety). Similarly, "reporter genes," which encode for enzymes providing for production of an identifiable compound are suitable. The most widely used reporter gene for gene fusion experiments has been uidA, a gene from Escherichia coli that encodes the β-glucuronidase protein, also known as GUS (Jefferson et al., "GUS Fusions: β Glucuronidase as a Sensitive and Versatile Gene Fusion Marker in Higher Plants," EMBO J., 6:3901-3907 (1987), which is hereby incorporated by reference in its entirety). Similarly, enzymes providing for production of a compound identifiable

by luminescence, such as luciferase, are useful. The selection marker employed will depend on the target species; for certain target species, different antibiotics, herbicide, or biosynthesis selection markers are preferred.

[0092] Plant cells and tissues selected by means of an inhibitory agent or other selection marker are then tested for the acquisition of the transgene by Southern blot hybridization analysis, using a probe specific to the transgenes contained in the given cassette used for transformation (Sambrook et al., "Molecular Cloning: A Laboratory Manual," Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press (1989), which is hereby incorporated by reference in its entirety).

[0093] After the expression cassette is stably incorporated in transgenic plants, it can be transferred to other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. Once transgenic plants of this type are produced, the plants themselves can be cultivated in accordance with conventional procedure so that the nucleic acid construct is present in the resulting plants. Alternatively, transgenic seeds or propagules (e.g., cuttings) are recovered from the transgenic plants. These seeds can then be planted in the soil and cultivated using conventional procedures to produce transgenic plants.

[0094] Thus, in other embodiments, the present invention includes transgenic plants and seeds produced by transformation with the nucleic acid molecule of the present invention which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant. Examples of transgenic plants include crop plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane. Other examples of transgenic plants include ornamental plants such as *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

[0095] The nucleic acid molecule of the present invention can be utilized to restore fertility to cytoplasmic male sterile plants for a wide variety of crop plants and ornamental plants. Thus, the present invention also relates to a method of restoring fertility to cytoplasmic male sterile plants involving transforming a cytoplasmic male

sterile plant with a nucleic acid molecule of the present invention under conditions effective to restore fertility to the cytoplasmic male sterile plant. The plant can have 2 or more copies of the nucleic acid molecule.

[0096] The nucleic acid molecule of the present invention can be utilized in a method for identifying genes affecting male fertility or mitochondrial gene expression in other species. The first PPR gene family member whose function was characterized is *crp1*, a gene involved in RNA processing in chloroplasts (Fisk et al., "Molecular Cloning of the Maize Gene crp1 Reveals Similarity Between Regulators of Mitochondrial and Chloroplast Gene Expression," EMBO J., 18: 2621-2630 (1999), which is hereby incorporated by reference in its entirety). *Rf-PPR592* and *crp1* exhibit some sequence similarity, though there are other PPR motif proteins in the databases with greater similarity to *Rf-PPR592*. Both of these genes affect accumulation of particular RNA transcripts.

[0097] Thus, another aspect of the present invention relates to a method of identifying a candidate gene restoring fertility in plants. The method involves analyzing the candidate gene for the presence of the above nucleic acid molecule in accordance with the present invention.

[0098] Identification of the nucleic acid molecules of the present invention suggests new strategies for identification of restorers or nuclear male sterility (ms) alleles in crop species that are more important agriculturally than petunia. Thus, another aspect of the present invention relates to a method of identifying a candidate plant suitable for breeding with a cytoplasmic male sterile plant. The method involves analyzing the candidate plant for the presence, in its genome, of the above nucleic acid molecule of the present invention.

[0099] For example, it is possible that a nucleic acid molecule of the present invention corresponds to a restorer allele in rice. Since the complete genome sequence of rice is publicly available, using the above-described method for identifying PPR motif-containing genes, candidates for rice restorer genes can be identified in the rice chromosomal region which is genetically linked to the rice restoration phenotype. Using standard methods of cloning and rice transformation, the candidate rice restorer gene can be introduced as a transgene into a rice CMS line and the fertility of the transformants can be evaluated to determine whether the PPR gene is actually a restorer gene.

[0100] The fact that the nucleic acid molecules of the present invention can be a PPR motif gene can also be used to identify putative genes in other species that might encode male sterility when disrupted. The homolog of a restorer gene in one species could, when mutated, be a male sterility-encoding gene in another species. Creating a male sterile line can be valuable for certain applications. For example, flowers of petunia and some other horticultural species undergo a phenomenon called pollination-induced senescence (Xu et al., "Programmed Cell Death During Pollination-Induced Petal Senescence in Petunia," Plant Phys., 122:1323-1333 (2000), which is hereby incorporated by reference in its entirety). Flowers are triggered to senesce when pollinated. A male sterile flower will last longer when the plant is male sterile, because no self pollen will be available to pollinate it.

[0101] Since it is possible to introduce genes into yeast mitochondria, it is likely that methods for introducing genes into plant mitochondria can be developed. When it becomes possible to introduce the *pcf* gene or a toxic homolog containing the sequences on which the nucleic acid molecule of the present invention operates, then a new CMS/restorer system can be created in a different species. In such a system, a male sterile line is created by introducing *pcf* or a *pcf* homolog into the mitochondrial genome. This CMS line can then be crossed with a line containing the nucleic acid molecule of the present invention in the nuclear genome, introduced by standard transformation methods, to create hybrid seed that will give rise to fertile progeny plants.

[0102] Thus, the present invention also relates to a method of producing hybrid plant seed. The method first involves providing a cytoplasmic male sterile plant. Next, a second plant containing the above nucleic acid molecule in accordance with the present invention is provided. Finally, the cytoplasmic male sterile plant and the second plant are bred under conditions effective to produce hybrid progeny seed which yield fertile plants.

[0103] Another aspect of the present invention relates to a method of producing plant seeds for an inbred line of plants. The method first involves providing a cytoplasmic male sterile plant. Next, a second plant containing the above nucleic acid molecule in accordance with the present invention is provided. Then, the cytoplasmic male sterile plant and the second plant are bred under conditions effective to produce hybrid progeny seed which yield fertile plants. Next, hybrid fertile plants

are produced from the hybrid progeny seeds Finally, the hybrid fertile plants and the second plant are backcrossed to produce seed which yield inbred progeny plants.

[0104] Backcrossing methods can be used with the present invention to improve or introduce a characteristic into the present cultivar. The term backcrossing refers to the repeated crossing of a hybrid progeny back to one of the parental plants for that hybrid. The parental plant which contributes the locus for the desired characteristic is termed the nonrecurrent or donor parent. This terminology refers to the fact that the nonrecurrent parent is used one time in the backcross protocol and, therefore, does not recur. The parental plant to which the locus or loci from the nonrecurrent parent are transferred is known as the recurrent parent as it is used for several rounds in the backcrossing protocol (Poehlman et al., Breeding Field Crops, 4th Ed., Ames, Iowa, Iowa State University Press, (1995); Fehr, ed., Principles of Cultivar Development, Vol. 1: Theory and Technique, NY, NY, Macmillan Publishing Company (1987); and Fehr, ed., Principles of Cultivar Development, Vol. 2: Crop Species, NY, NY, Macmillan Publishing Company (1987), which are hereby incorporated by reference in their entirety).

[0105] In a typical backcross protocol, the phenotypically and/or commercially appealing cultivar or accession (recurrent parent) is crossed with a second cultivar (nonrecurrent parent) that carries the single locus of interest (e.g., the GSB resistance gene locus) to be transferred. The resulting progeny from this cross are then crossed again to the recurrent parent and the process is repeated until a plant is obtained where essentially all of the desired morphological and physiological characteristics of the recurrent parent are recovered in the converted plant, in addition to the single transferred locus from the nonrecurrent parent.

[0106] The selection of a suitable recurrent parent is an important step for a successful backcrossing procedure. The goal of a backcross protocol is to alter or substitute a single trait or characteristic in the original cultivar or accession. To accomplish this, a single locus of the recurrent cultivar is modified or substituted with the desired locus from the nonrecurrent parent, while retaining essentially all of the rest of the desired genetic, and therefore the desired physiological and morphological constitution of the original cultivar. The choice of the particular nonrecurrent parent will depend on the purpose of the backcross; one of the major purposes is to add some commercially desirable, agronomically important trait to the plant. The exact

backcrossing protocol will depend on the characteristic or trait being altered to determine an appropriate testing protocol. Although backcrossing methods are simplified when the characteristic being transferred is a dominant allele, a recessive allele may also be transferred. In this instance it may be necessary to introduce a test of the progeny to determine if the desired characteristic has been successfully transferred.

[0107] A technique, known as modified backcrossing, uses different recurrent parents during the backcrossing. Modified backcrossing may be used to replace the original recurrent parent with a cultivar having certain more desirable characteristics or multiple parents may be used to obtain different desirable characteristics from each.

[0108] Presently, it is possible to introduce genes into chloroplast genomes, which are maternally inherited in many species. Therefore, a CMS/restorer system can also be created by introducing the *pcf* locus, modified for chloroplast expression, into the chloroplast genome. The nucleic acid molecule of the present invention can be modified to replace the mitochondrial transit sequence with a chloroplast transit sequence, using standard methods (Kohler et al., "Exchange of Protein Molecules Through Connections Between Higher Plant Plastids," Science, 276:2039-2042 (1997), which is hereby incorporated by reference in its entirety), so that the protein encoded by the nucleic acid molecule of the present invention will turn off toxic gene expression in the chloroplast. Without the restorer, PCF in the chloroplast is likely to be toxic; PCF is toxic to *E. coli* bacteria. Thus, the present invention also relates to a method of producing plants with a cytoplasmic male sterile plant restoration system. The method first involves transforming a first plant in its chloroplast genome with a nucleic acid which causes the plant to become male sterile. Next, a second plant is transformed with the above nucleic acid molecule in accordance with the present invention whose protein product is targeted to the chloroplast. Finally, the first and second plants are crossed to produce progeny plants possessing a cytoplasmic male sterile plant restoration system.

[0109] Since the nucleic acid molecule of the present invention prevents the expression of an organelle gene, it can be used to control the expression of a chimeric gene introduced into chloroplasts. If there is a useful protein that is desired to be produced from plant chloroplasts by introduction of a gene encoding the valuable

protein into the chloroplast genome, production of the valuable protein could deliberately be turned off by expressing the nucleic acid molecule of the present invention from a conditional promoter. When desired, the expression of the nucleic acid molecule of the present invention could be turned off, so that the valuable protein is produced. In further detail, the method of the present invention involves: (1) engineering a chimeric gene including the coding region of a desirable protein and the *pcf* gene sequences that are regulated by the nucleic acid molecule of the present invention; (2) introducing this chimeric gene into chloroplasts of a plant and obtaining a chloroplast transgenic line; (3) engineering the nucleic acid molecule of the present invention or its homologs so that the protein is targeted into chloroplasts; (4) introducing the engineered nucleic acid molecule of the present invention into the nuclear genome of a plant and obtaining a nuclear transgenic line; and (5) crossing plants to set up a regulated system. Alternatively, the plant in (2) can be made first and the gene in (3) introduced by transformation, or the plant in (4) can be made first and the gene in (2) introduced into the plant in (4). When it becomes possible to transform plant mitochondrial genomes, the chimeric gene containing the *pcf* sequence can be introduced into mitochondria and the product of the nucleic acid molecule of the present invention can be targeted to mitochondria to create the analogous system.

[0110] The nucleic acid molecule of the present invention must be expressed in most of the plant, because in every tissue examined, the PCF protein is reduced in the presence of the nucleic acid molecule of the present invention (Nivison et al., "Identification of a Mitochondrial Protein Associated With Cytoplasmic Male Sterility in *Petunia*," Plant Cell, 1:1121-30 (1989), Nivision et al., "Sequencing, Processing, and Localization of the *Petunia* CMS-Associated Mitochondrial Protein," Plant J., 5:613-623 (1994), which are hereby incorporated by reference in their entirety). The PCF protein does nevertheless vary in abundance (Conley et al., "Tissue-Specific Protein Expression in Plant Mitochondria," Plant Cell, 6:85-91 (1994), which is hereby incorporated by reference in its entirety) and is more highly expressed in anthers. Very few promoters have been identified that confer expression in many tissues and in developing microspores at an early stage of pollen development. Thus, the promoter sequence of the nucleic acid molecule of the

present invention could be useful to express any of many different coding regions in a variety of tissues.

[0111] It is also possible to dissect the regulatory sequences of the nucleic acid molecule of the present invention by standard methods to identify those regions that confer expression in particular tissue types. Typically, such regulatory sequences are 5' to the coding region, though the 3' flanking region can also be important. The most novel aspect of the regulatory sequences of the nucleic acid molecule of the present invention is that they confer expression in early microsporogenesis. Most of the published anther-specific promoters are not effective at the early stage of pollen development, when it is critical to restore proper mitochondrial function in plants carrying the CMS cytoplasm. For example, the promoter of a nucleic acid molecule of the present invention could be used with a different coding region to restore fertility to a species with a different CMS-encoding gene. Alternatively, the promoter could be used to control a gene toxic to pollen to confer male sterility, or regulatory elements from this promoter could be combined with those of another promoter to confer expression in early microsporogenesis.

[0112] Thus, another aspect of the present invention relates to a method of directing gene expression to plant mitochondria. The method involves transforming a plant with a chimeric nucleic acid molecule containing a transgene operatively linked to a promoter or a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant. The promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1. The terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

[0113] The present invention also relates to a promoter from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant. The promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1.

[0114] Another aspect of the present invention relates to a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to

direct expression of the transgene in the mitochondria of the transformed plant. The terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

[0115] Another aspect of the present invention relates to a nucleic acid construct. The nucleic acid construct includes: (i) a promoter or a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant and (ii) a nucleic acid heterologous to and operatively coupled to the promoter or the terminator. The promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1. The terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

[0116] Other embodiments of the present invention include isolated expression systems, host cells, transgenic plants, and transgenic plant seeds containing the nucleic acid construct of the present invention.

[0117] Another aspect of the present invention is a method of expressing a gene preferentially in roots of a plant. The method involves transforming a plant with a nucleic acid construct containing a promoter suitable for driving expression preferentially in roots having a nucleotide sequence of from 1 to 1388 of SEQ ID NO: 44; a nucleic acid heterologous to the promoter, where the promoter is operatively coupled 5' to the nucleic acid to induce transcription of the nucleic acid; and a terminator having a nucleotide sequence of from nucleotide 3168 to 4016 of SEQ ID NO: 44, where the terminator is operably coupled 3' to the nucleic acid. This method can be used to express genes in roots of a plant, but not in stems, leaves, or buds.

[0118] The nucleic acid molecule of the present invention or its homologues could also be used to deliberately alter floral morphology to produce novel flowers. Thus, in another embodiment, the present invention is a method of altering plant floral morphology in ornamental plants by transforming an ornamental plant with a nucleic acid molecule of the present invention which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant. Combinations of certain nuclear genes with particular mitochondrial backgrounds have been found to result in altered floral morphology in some genera. For example, in tobacco, combinations of the nuclear genome of one species with the cytoplasm of

another sometimes results in very abnormal flowers, such as flowers in which anthers have been converted to petals. While these particular plants may not be desirable horticulturally, it is possible that the coding region or expression of the nucleic acid molecule of the present invention could be manipulated so that interesting, valuable floral alterations could be obtained. For example, flowers with a second set of petals in place of anthers could be attractive. A similar strategy could be pursued with other species in which novel floral morphology is desirable. Manipulation of the nucleic acid molecule of the present invention could occur, for example, by overexpressing it on a different promoter, changing the coding region, or using standard antisense or gene silencing methods to underexpress homologous genes.

[0119] Another aspect of the present invention relates to a method of producing plants with a cytoplasmic male sterile plant restoration system. The method first involves mutagenizing a first plant having a nucleic acid which encodes a protein. The protein has a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input. Next, the mutagenized first plant is crossed with a wild-type plant having mitochondrial DNA polymorphisms compared to mitochondrial DNA in the mutagenized first plant to produce progeny plants. Finally, it is determined if the progeny plants are fertile, whereby fertile progeny plants can be used as a fertile maintainer line, where the mutagenized first plant, the fertile maintainer line, and a wild-type allele present in the first plant before mutagenesis comprises a new cytoplasmic male sterile plant restoration system. Figures 7A-B show this aspect of the present invention in detail.

[0120] The *Arabidopsis thaliana* genome sequence contains a PPR gene highly similar to the nucleic acid molecule of the present invention. There are existing, publicly available insertional element collections that can be screened by standard methods to find a mutant in which the homolog of the nucleic acid molecule of the present invention is disrupted. The mutant can be examined to determine whether it encodes male sterility. Because the nucleic acid molecule of the present invention is important for nuclear/organelle interaction to produce male fertility, its

homologs in other species are likely to be essential for proper pollen development in those species.

[0121] By mutating a PPR gene in a plant that does not have a CMS/restorer system, such a system can be created. In this strategy, a PPR gene is mutated and the plant becomes male sterile. The mutated PPR alleles are then crossed with plants carrying other cytoplasms, present in other varieties of the plant or in intercrossable species. If a cytoplasm can be found in which the plant is fertile in the presence of the two mutated PPR alleles, then a new CMS/restorer system will have been created. A line carrying the new cytoplasm plus the mutated alleles becomes the maintainer line. The line carrying the first cytoplasm plus the mutated alleles becomes *rf/rf* CMS. A line carrying an unmutated allele plus a mutated allele in the presence of the CMS cytoplasm becomes *Rf/rf* CMS. These lines can then be exploited just as standard maintainer, sterile, and restored lines are currently used in hybrid seed production (Figure 7).

[0122] For example, tomato does not have a CMS/restorer system. It is known that markers near petunia *Rf* map to a region of the tomato genome where two nuclear male sterility alleles exist. Possibly, the tomato ortholog of the nucleic acid molecule of the present invention, when mutated, results in male sterility. If so, then the cytoplasms of the intercrossable wild tomato species can be tested to determine whether they can confer male fertility to a tomato line homozygous for the mutated PPR gene.

[0123] The nucleic acid molecule of the present invention may not be usable directly to restore fertility to CMS lines of most other species. Current information indicates that different mitochondrial genes are present in different CMS lines. In most cases, restorer genes will have a specific mechanism of action—suppression of expression of the abnormal mitochondrial gene. However, by chance, there may be a few species that carry a CMS cytoplasm whose abnormality can be ameliorated by the nucleic acid molecule of the present invention. This can be determined by introducing the nucleic acid molecule of the present invention into the other species and determining whether the transgenic plants become male fertile. If so, the nucleic acid molecule of the present invention can be used as a fertility restorer for this species.

EXAMPLES

[0124] The following examples are provided to illustrate embodiments of the present invention but are by no means intended to limit its scope.

Example 1 – Identification of Two PPR-Containing ORFs as Potential Candidates for the *Rf* Gene

[0125] Previously, the isolation of a 37.5-kb BIBAC clone, SB5, that cosegregates with the Rf gene has been reported (Bentolila et al., "Identification of a BIBAC Clone That Co-Segregates With the Petunia Restorer of Fertility (Rf) Gene," Mol. Genet. Genomics, 266:223-230 (2001), which is hereby incorporated by reference in its entirety). SB5 is part of a contig that was constructed by screening a Petunia BIBAC library with a marker, EACA/MCTC, tightly linked to Rf. No recombination was identified between EACA/MCTC and Rf after examining 1,078 meiotic events. The genetic delimitation of the Rf locus was achieved only partially on the BIBAC contig. One extremity of the contig was separated from Rf by the occurrence of four recombination events, whereas no crossing-over was found between Rf and the other extremity (Bentolila et al., "Identification of a BIBAC Clone That Co-Segregates With the Petunia Restorer of Fertility (Rf) Gene," Mol. Genet. Genomics, 266:223-230 (2001), which is hereby incorporated by reference in its entirety). Because of the possibility that Rf might lie further away in the area not covered by the contig, a walk was initiated by screening the BIBAC library with a probe lying on the extremity that cosegregates with Rf. Unfortunately, the only hits were clones already isolated in the contig, demonstrating the presence of a gap in the Petunia BIBAC library.

[0126] Before increasing the redundancy of the library to find new clones covering the gap, it was determined whether the Rf gene might lie in the SB5 clone. Because the BIBAC vector is a binary vector allowing Agrobacterium-mediated plant transformation (Hamilton, "A Binary-BAC System for Plant Transformation With High-Molecular-Weight DNA," Gene, 200:107-116 (1997), which is hereby incorporated by reference in its entirety), SB5 was used to restore fertility to CMS plants. Unfortunately, although SB5 is stable in E. coli, it underwent multiple rearrangements when introduced into A. tumefaciens, thus precluding its use in

transgenic experiments. Randomly chosen clones of various sizes did not show this instability in A. tumefaciens, pointing to special features in the sequence of the SB5 insert.

[0127] To address whether Rf might lie in the SB5 clone, shotgun sequencing of the entire clone was carried out and the predicted ORFs for candidate Rf genes were examined.

[0128] Because of difficulties in contig assembly caused by the presence of repeated sequences, BamHI subclones rather than the entire BIBAC clone were used as the starting material for shotgun sequencing. DNA was sonicated into 1- to 3-kb fragments, which were gel purified (Geneclean Spin Kit, Bio 101, Vista, CA), end-repaired with T4 DNA polymerase (GIBCO/BRL, Rockfield, MD) in the presence of all four dNTPs, and ligated at a mass ratio of 3 inserts to 1 vector into the SmaI site of the pTrueBlue vector (Genomics One, Buffalo, NY). The ligation product was introduced into Electromax DH10B Escherichia coli cells (GIBCO/BRL), and DNA obtained from the white colonies by minipreparation was sequenced with the T7 primer in the Cornell BioResource Center. The sequences were assembled into contigs with SEQUENCHER (Gene Codes, Ann Arbor, MI).

[0129] ORFs from BIBAC SB5, their promoter region, and poly(A) signals were predicted by using GENSCAN (Burge et al., "Prediction of Complete Gene Structures in Human Genomic DNA," J. Mol. Biol., 268:78-94 (1997), which is hereby incorporated by reference in its entirety) with the Arabidopsis parameter matrix. Duplicated blocks in the Rf locus were determined by aligning the genomic sequence against itself by using the dot-plot feature from the MEGALIGN program (DNAstar, Madison, WI) with a 90% match. The presence of a transit peptide in the ORFs was determined by using PREDOTAR version 0.5 , TARGETP (Emanuelsson et al., "Predicting Subcellular Localization of Proteins Based on Their N-Terminal Amino Acid Sequence," J. Mol. Biol., 300:1005-1016 (2000); Nielsen et al., "Identification of Prokaryotic and Eukaryotic Signal Peptides and Prediction of Their Cleavage Sites," Prot. Eng., 10:1-6 (1997), which are hereby incorporated by reference in their entirety), and MITOPROT (Scharfe et al., Nucleic Acids Res., 28:155-158 (2000), which is hereby incorporated by reference in its entirety). The length of the transit peptide was predicted by TARGETP and MITOPROT.

[0130] PPR motifs were identified in Rf-PPR592 and Rf-PPR591 by the MEME software (Bailey et al., in "Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology," in Altman, eds. (Am. Assoc. Artificial Intelligence Press, Menlo Park, CA), pp. 28-36 (1994), which is hereby incorporated by reference in its entirety). The parameters for motif searching were set as minimum width = 35, maximum width = 35. The PPR consensus motif computed from the comparison of 1,303 motifs has been described previously (Small et al., "The PPR Motif - A TPR-Related Motif Prevalent in Plant Organellar Proteins," Trends Biochem. Sci., 25:46-47 (2000), which is hereby incorporated by reference in its entirety).

[0131] Because the Rf gene is expected to be targeted to mitochondria where it can act upon the pcf gene to prevent its expression, an ORF predicted to carry mitochondrial transit sequences was searched. Two ORFs with putative mitochondrial targeting signals were identified. The two ORFs are adjacent to each other and appear to have originated from duplications in the promoter and coding region, but carry divergent 3' flanking regions (Figure 1A). The ORFs were 92% identical at the nucleotide level, and the predicted proteins were 93% similar, with C termini that differ completely in their final 12 aa. Both ORFs carry PPR motifs; one encodes 591 aa and the other encodes 592 aa, and were therefore named Rf-PPR591 and Rf-PPR592. A third PPR-containing ORF might lie in the vicinity of the two PPR-containing ORFs shown in Figure 1A. On the left extremity lies a genomic block that shares high similarity with the end of the coding sequence of Rf-PPR592 and its terminator region.

[0132] According to cleavage prediction programs, both putative proteins exhibited 28-residue mitochondrial transit peptides. Predicted transit peptides of Rf-PPR592 and Rf-PPR591 differed by only one substitution. To determine whether the predicted transit peptide could target a passenger protein to mitochondria, 44 codons from the 5' end of the Rf-PPR592 coding region were inserted 5' to the coding region of an enhanced GFP. DNAs of this construct and of one known to target GFP to mitochondria were bombarded into onion epidermal cells. Both GFPs appeared to be localized to the same type of organelle in the single cells shown in Figures 1B and C. Because the predicted transit peptides of Rf-PPR592 and Rf-PPR591 differed by only

one amino acid, it was expected that not only Rf-PPR592 but also Rf-PPR591 would be mitochondrially localized.

[0133] Most of the predicted mature protein (87%) of Rf-PPR592 consisted of 14 PPRs (Figure 1D). These repeats extended from the amino acid in position 54 to the amino acid in position 544 and are organized in two sets of tandem repeats, one set containing 3 PPRs from amino acid 54 to amino acid 158, the other set containing 11 PPRs from amino acid 160 to amino acid 544. Because the Rf-PPR591 and Rf-PPR592 proteins are 93% similar and differ mainly in the last 12 C-terminal amino acids, their organization with respect to PPRs is identical. There was a very good agreement between the consensus motif derived from the 14 PPRs found in Rf-PPR592 (hereafter designated 14 PPR consensus) and the consensus motif derived from 1,303 PPRs (hereafter designated 1303 PPR consensus) reported previously (Small et al., "The PPR Motif - A TPR-Related Motif Prevalent in Plant Organellar Proteins," Trends Biochem. Sci., 25:46-47 (2000), which is hereby incorporated by reference in its entirety) (Figure 1D). Whenever a discrepancy occured between the consensus motif of the 14 PPRs in Rf-PPR592 and the 1303 PPR consensus, the difference usually was a conservative substitution. For instance, the aspartic acid in the first position of the 14 PPR consensus is replaced by a glutamic acid in the 1303 PPR consensus. Moreover, when the most frequent amino acid in the 14 PPR consensus at a given position differed from the corresponding amino acid found in the 1303 PPR consensus, the amino acid in the 1303 consensus was generally the second most frequent in the 14 PPR consensus (glutamic acid at position 1, asparagine at position 18, alanine at position 28, tyrosine at position 29; Figure 1D).

[0134] It has been demonstrated that *Rf-PPR592*, a gene encoding a 592-aa protein containing 14 PPRs, was able to restore fertility to CMS plants. The PPR motif, a degenerate 35-aa repeat, has been found in a very large gene family in the *Arabidopsis* genome (Small et al., "The PPR Motif - A TPR-Related Motif Prevalent in Plant Organellar Proteins," Trends Biochem. Sci., 25:46-47 (2000), which is hereby incorporated by reference in its entirety). The repeats are organized in tandem arrays with the number of motifs per peptide ranging from 2 to 26. About two-thirds of these *Arabidopsis* PPR proteins are predicted to be targeted to either mitochondria or chloroplasts (Small et al., "The PPR Motif - A TPR-Related Motif Prevalent in Plant Organellar Proteins," Trends Biochem. Sci., 25:46-47 (2000), which is hereby

incorporated by reference in its entirety). Although distinct from the tetratricopeptide repeat (TPR), a motif that is likely to be involved in protein binding, the PPR motif shares with the former a predicted spatial structure consisting of two α-helices (Small et al., "The PPR Motif - A TPR-Related Motif Prevalent in Plant Organellar Proteins," Trends Biochem. Sci., 25:46-47 (2000); Das et al., "The Structure of the Tetratricopeptide Repeats of Protein Phosphatase 5: Implications for TPR-Mediated Protein-Protein Interactions," EMBO J., 17:1192-1199 (1998), which are hereby incorporated by reference in their entirety). Tandem PPRs are thought to form a superhelix with a central spiral groove that presumably serves as the ligand-binding surface in a similar way as the one predicted for the tandem TPRs (Small et al., "The PPR Motif - A TPR-Related Motif Prevalent in Plant Organellar Proteins," Trends Biochem. Sci., 25:46-47 (2000), which is hereby incorporated by reference in its entirety). However, unlike in the TPR motif, the side chains lining the central groove of the PPR are almost exclusively hydrophilic, suggesting that some or all of the PPR motifs are RNA-binding rather than protein-binding motifs. This hypothesis is supported by the involvement in RNA metabolism and/or translation of the very few PPR motif-containing proteins characterized so far: maize chloroplast CRP1, involved in chloroplast *petD* RNA processing and *petD* and *petA* translation (Fisk et al., "Molecular Cloning of the Maize Gene *Crp1* Reveals Similarity Between Regulators of Mitochondrial and Chloroplast Gene Expression," EMBO J., 18:2621-2630 (1999), which is hereby incorporated by reference in its entirety), *Chlamydomonas* MCA1, required for the accumulation of the chloroplast *petA* transcript (Lown et al., "Chlamydomonas Nuclear Mutants That Fail to Assemble Respiratory or Photosynthetic Electron Transfer Complexes," Biochem. Soc. Trans., 29:452-455(2001), which is hereby incorporated by reference in its entirety), yeast PET309, required for the stability and translation of the *coxI* mitochondrial mRNA (Manthey et al., "The Product of the Nuclear Gene PET309 is Required for Translation of Mature mRNA and Stability or Production of Intron-Containing RNAs Derived from the Mitochondrial COX1 Locus of Saccharomyces cerevisiae," EMBO J., 14:4031-4043 (1995), which is hereby incorporated by reference in its entirety), and *Drosophila* BSF, which binds to and stabilizes the bicoid mRNA (Mancebo et al., "BSF Binds Specifically to the *bicoid* mRNA 3' Untranslated Region and Contributes to Stabilization of *bicoid* mRNA," Mol. Cell. Biol., 21:3462-3471 (2001), which is

hereby incorporated by reference in its entirety). That *Petunia Rf* belongs to this family is consistent with its similarity of action to *crp1*, *mca1*, and *pet309*. Mutations in these three genes result in lack of accumulation of a particular transcript and reduced abundance of an organelle protein. Likewise, in *Petunia* restored plants, among the population of *pcf* transcripts with different 5' termini, the ones with termini at -121 exhibit reduced abundance and the amount of the PCF protein is greatly reduced (Pruitt et al., "Transcription of the Petunia mitochondrial CMS-Associated Pcf Locus in Male Serile and Fertility-Restored Lines," Mol. Gen. Genet., 227:348-355 (1991); Nivison et al., "Identification of a Mitochondrial Protein Associated with Cytoplasmic Male Sterility in Petunia," Plant Cell, 1:1121-1130 (1989), which are hereby incorporated by reference in their entirety). However, the alleles of the other PPR genes that are known to reduce RNA and/or protein accumulation are recessive, whereas the *Petunia Rf* allele is dominant. *Rf* genes from other species have been shown to alter the RNA transcript profile of the CMS-associated genes (Wise et al., "Mutator-Induced Mutations of the rf1 Nuclear Fertility Restorer of T-Cytoplasm Maize Alter the Accumulation of T-urf13 Mitochondrial Transcripts," Genetics, 143:1383-1394 (1996); Singh et al., "Suppression of Cytoplasmic Male Sterility by Nuclear Genes Alters Expression of a Novel Mitochondrial Gene Region," Plant Cell, 3:1349-1362 (1991); Tang et al., "Transcript Processing Internal to a Mitochondrial Open Reading Frame is Correlated with Fertility Restoration in Male-Sterile Sorghum," Plant J., 10:123-133 (1996); Moneger et al., "Nuclear Restoration of Cytoplasmic Male Sterility in Sunflower is Associated with the Tissue-Specific Regulation of a Novel Mitochondrial Gene," EMBO J., 13:8-17 (1994), which are hereby incorporated by reference in their entirety). In some cases, restoration has been shown to result from enhanced processing of the CMS-associated transcripts (Tang et al., "Transcript Processing Internal to a Mitochondrial Open Reading Frame is Correlated with Fertility Restoration in Male-Sterile Sorghum," Plant J., 10:123-133 (1996); Menassa et al., "Post-Transcriptional and Developmental Regulation of a CMS-Associated Mitochondrial Gene Region by a Nuclear Restorer Gene," Plant J., 17:491-499 (1999), which are hereby incorporated by reference in their entirety). Taken together, these observations suggest that *Rf*s in other species could also be PPR-containing genes like the *Petunia Rf*.

[0135] The data presented here show that a pair of duplicated PPR-containing genes, denoted *Rf-PPR591* and *Rf-PPR592*, lie in the *Petunia Rf* locus. A third related PPR gene might lie in the area not covered by the SB5 BIBAC clone as suggested by the high similarity between the sequence available at the end of the clone and the sequence present at the end of the coding sequence of *Rf-PPR592* and in its terminator region.

[0136] In *Brassica napus*, the restorer locus has been shown to affect the transcripts of several mitochondrial genes, two of them being associated with the *nap* and *pol* CMS (Singh et al., "Nuclear Genes Associated With a Single Brassica CMS Restorer Locus Influence Transcripts of Three Different Mitochondrial Gene Regions," Genetics, 143:505-516 (1996); Li et al., "Restorer Genes for Different Forms of *Brassica* Cytoplasmic Male Sterility Map to a Single Nuclear Locus That Modifies Transcripts of Several Mitochondrial Genes," Proc. Natl. Acad. Sci. USA, 95:10032-10037 (1998), which are hereby incorporated by reference in their entirety). At the same locus have been mapped *Rfp*, the restorer gene to the *pol* CMS, that modifies the transcripts of the *pol* CMS-associated *orf224/atp6* mitochondrial DNA region, *Rfn*, the restorer gene to the *nap* CMS that modifies the transcripts of the *nap* CMS-associated *orf222/nad5c/orf139* mitochondrial DNA region, and *Mmt* (modifier of mitochondrial transcripts), a gene that modifies the transcripts of the *nad4* gene and another gene possibly involved in cytochrome *c* biogenesis (Li et al., "Restorer Genes for Different Forms of *Brassica* Cytoplasmic Male Sterility Map to a Single Nuclear Locus That Modifies Transcripts of Several Mitochondrial Genes," Proc. Natl. Acad. Sci. USA, 95:10032-10037 (1998), which is hereby incorporated by reference in its entirety). The resolution of the genetic mapping in these studies did not allow the authors to address whether the three genes represent different alleles of a single gene or whether the restorer locus might contain multiple, related, tightly linked genes. A similar situation occurs in *Sorghum,* where at the *Rf3* locus, one of the two restorers to A3 CMS, has been mapped a gene that regulates the transcript-processing activity of A3 CMS-associated *orf107* and the *Mmt1* gene that enhances the transcript processing of *urf209* (Tang et al., "Cosegregation of Single Genes Associated with Fertility Restoration and Transcript Processing of Sorghum Mitochondrial *orf107* and *urf209*," Genetics, 150:383-391 (1998), which is hereby incorporated by reference in its

entirety). As in *Brassica napus*, either a multiallelic model or tightly linked genes could account for this result.

[0137] It will be worthwhile to determine whether *Rf-PPR591* affects the profile of mitochondrial transcripts other than *pcf* in transgenic plants. If so, it would strengthen the hypothesis that *Rf* alleles arise as modifications, perhaps through duplication, of existing alleles that control mitochondrial gene expression. According to this theory, once CMS occurs in a plant species, there may be strong selective pressure for the plant to overcome it by recruiting preexisting activities and redirecting them to down-regulate the expression of CMS-encoding genes. Conceivably, recombination among closely related PPR-containing genes could have led to the appearance of the *Rf-PPR592* gene.

Example 2 - A Deletion in the Promoter of *rf-PPR592* Prevents Its Expression in CMS Floral Buds

[0138] If one of the candidate ORFs, Rf-PPR591 or Rf-PPR592, is the Rf gene, some sequence polymorphism between the allele of these ORFs found in a restorer line (Rf/Rf) and the allele found in a CMS plant (rf/rf) might be expected. Presumably some difference in the sequences of the dominant Rf allele vs. the recessive nonrestoring allele rf must reflect their opposite restoring ability. The sequence of rf-PPR592 was obtained by amplifying genomic DNA of a Petunia hybrida rf/rf plant, where rf was inherited from a P. hybrida line called 2423, with the PfuTurbo Hotstart DNA polymerase (Stratagene, La Jolla, CA) and PCR primers flanking Rf-PPR591 (5'-TGCACAGTGTTATATTTACATACCC-3'; SEQ ID NO: 46) and Rf-PPR592 (5'-TTTATGATACATGGATTTCAACGAC-3'; SEQ ID NO: 47). A PCR product was obtained only with a primer specific to the 3' flanking region of Rf-PPR592, not with a primer specific to the 3' flanking region of Rf-PPR591. The rf-PPR592 PCR product showed a reduction in size of about 500nt compared with the Rf-PPR592 PCR product amplified from the genomic DNA of an Rf/Rf line (Figure 2A). Using the same primers, a PCR product similar in size to rf-PPR592 was amplified from another nonrestoring P. hybrida line as well as from a nonrestoring Petunia parodii line. The rf-PPR592 PCR product amplified from the P. hybrida 2423 sequence was cloned into the pCR-Blunt II-TOPO vector (Invitrogen, Carlsbad, CA) and sequenced, revealing a gene 97% identical to Rf-PPR591 and 94% identical

to Rf-PPR592 in the coding region, with the predicted proteins 98% and 94% similar, respectively. Because of the primer design, the rf-PPR592 sequence lacks 35 nt available for Rf-PPR592. Similarity blocks between rf-PPR592, Rf-PPR592, and Rf-PPR591 were determined by comparing the aligned sequences with SEQUENCHER. Percent similarity was computed by using the MEGALIGN program. Comparison of the similarities of regions of the three different PPR genes revealed that the 5' promoter region of rf-PPR592 is most similar to Rf-PPR591, whereas the 3' flanking region of rf-PPR592 is most similar to Rf-PPR592. The genomic structure of rf-PPR592 was consistent with the past occurrence of recombination between two genes similar to Rf-PPR591 and Rf-PPR592 (Figure 2B). Because PCR amplification could have resulted in an artificial recombination between Rf-PPR591 and Rf-PPR592 due to their high similarity, the Rf-PPR592 PCR product was resequenced as a control experiment. The sequences of three rf-PPR592 and Rf-PPR592 clones were determined. No evidence of recombination was found in any of the sequenced Rf-PPR592 clones, thus precluding PCR amplification as the source of the genetic mosaic found in the rf-PPR592 ORF.

[0139] rf-PPR592 carries a 530-nt deletion from -556 to -27 relative to the start codon of Rf-PPR592. This deletion is responsible for the observed difference in the sizes of the respective amplicons. Rf-PPR591 has a 49-nt gap within the same region, from -273 to -224 relative to the start codon of Rf-PPR592 (Figure 2B).

[0140] RT-PCR experiments were performed to determine whether both Rf-PPR592 and rf-PPR592 are expressed in Petunia floral buds. The RT reaction was performed with Superscript II RNase H- reverse transcriptase (GIBCO), and the PCR was performed with the PfuTurbo Hotstart DNA polymerase. The reverse primer R3 used for reverse transcription (RT)-PCR lies in the 3' untranslated region of the Rf-PPR592 gene at position +430 to +454. The forward primer used for the PCR lies in the coding sequence and is specific to the rf or Rf allele, F2S or F2, respectively, because of DNA polymorphisms between rf and Rf in this area. Primer pairs F2SR3 amplified a 1333-bp product and F2R3 amplified a 1507-bp product. R3, 5'-TGAAAATGACAATCGTAACAGAAAA-3' (SEQ ID NO: 48); F2, 5'-AACATTCCTCCAGACATTATTACA-3' (SEQ ID NO: 49); F2S, 5'-GACGCTGAGGAAATAATGAGATAC-3' (SEQ ID NO: 50).

[0141] An Rf-PPR592 transcript was detected in floral buds in lines carrying the Rf allele, but no transcripts of rf-PPR592 were detected in a homozygous nonrestoring rf/rf line (Figure 3A). The absence of the upstream 530-nt region in rf-PPR592 is likely to prevent the expression of PPR592 in the floral buds of nonrestoring lines.

[0142] Since rf-PPR592 encodes a protein that is very similar to the one encoded by Rf-PPR592, a survey of its expression was conducted in tissues other than the floral buds. From all of the tissues analyzed, an rf-PPR592 transcript was detected only in roots of a nonrestoring rf/rf line (Figure 3B).

[0143] A deletion of 530 nt in the promoter area of the *rf-PPR592* gene is the likely cause of its nonexpression in the floral buds of CMS plants. That the *rf-PPR592* gene, which encodes a protein 98% similar to Rf-PPR591 and 94% similar to Rf-PPR592, has not yet accumulated missense mutations suggests either a recent deletion in the promoter or a functional expression in plant organs other than the floral buds. This latter possibility was supported by the finding of an *rf-PPR592* transcript in the roots of homozygous nonrestoring *rf/rf* line.

[0144] Sequence inspection demonstrated that a recombination event between two genes similar to *Rf-PPR591* and *Rf-PPR592* can explain the formation of *rf-PPR592*. Perhaps once *Rf-PPR592* was generated and happened to prevent the expression of *pcf*, its maintenance required the presence of the CMS-associated gene. The absence of the CMS-associated gene in new nucleocytoplasmic combinations might have resulted in recombination between *Rf-PPR591* and *Rf-PPR592* because of their high similarity. In *Brassica* and related genera, *Rfn* is found only in association with the *nap* cytoplasm, suggesting that the evolutionary appearance of the *nap* cytoplasm and the attending male sterility may have provided the selective pressure for the origin, and possibly the continued presence, of *Rfn* in *B. napus* (Li et al., "Restorer Genes for Different Forms of *Brassica* Cytoplasmic Male Sterility Map to a Single Nuclear Locus That Modifies Transcripts of Several Mitochondrial Genes," Proc. Natl. Acad. Sci. USA, 95:10032-10037 (1998), which is hereby incorporated by reference in its entirety). Sampling of more *rf-PPR592* genes from different *Petunia* species should help in understanding the evolution of CMS and fertility restoration in this genus.

Example 3 – *Rf-PPR592* Is Able to Restore Fertility to CMS Plants

[0145] A sequence encoding the N-terminal 44 aa of Rf-PPR592 was inserted 5' to the green fluorescent protein (GFP) sequence in the pOL vector (Peeters et al., "Duplication and Quadruplication of Arabidopsis Thaliana Cysteinyl- and Asparaginyl-tRNA Synthetase Genes of Organellar Origin," J. Mol. Evol., 50:413-423 (2000), which is hereby incorporated by reference in its entirety) to use in transient assay of protein localization. As a control, a vector carrying GFP fused with a known mitochondrial coxIV transit peptide (Akashi et al., "Potential Dual Targeting of an Arabidopsis Archaebacterial-Like Histidyl-Trna Synthetase to Mitochondria and Chloroplasts," FEBS Lett., 431:39-44 (1998), which is hereby incorporated by reference in its entirety) was also used in the transient assays. DNAs of GFP constructs were bombarded into onion epidermal cells as described in Scott et al., "Model System For Plant Cell Biology: GFP Imaging In Living Onion Epidermal Cells," BioTechniques, 26:1125, 1128-1132 (1999), which is hereby incorporated by reference in its entirety.

[0146] For the stable transformation experiments, genomic DNA from the Rf-PPR592 gene was amplified from the SB5 BIBAC clone with the PfuTurbo Hotstart DNA polymerase and the primers F11-XbaI (5'-TCTAGAAAAAATGAAGGGGGAATCAAT-3'; SEQ ID NO: 51) and R11-EcoRI (5'-GAATTCACTTTGCTCTCACGATAAACTAAGA-3';SEQ ID NO: 52) (underlined are the restriction sites added to the 5' end of the primers for further use in the cloning of the PCR product). The PCR product was first cloned into the pCR-Blunt II-TOPO vector, and its sequence was checked to be free of possible mutations generated by the polymerase. The PCR product was then released from the pCR-Blunt II-TOPO vector by digestion with XbaI and EcoRI, gel purified, and cloned into XbaI/EcoRI-digested binary vector pGPTVKan (Becker et al., "New Plant Binary Vectors With Selectable Markers Located Proximal to the Left T-DNA Border," Plant Mol. Biol., 20:1195-1197 29 (1992), which is hereby incorporated by reference in its entirety). Petunia transformation and regeneration were performed as described in Horsch et al., "A Simple and General-Method for Transferring Genes Into Plants," Science, 227:1229-1231 30 (1985), which is hereby incorporated by reference in its entirety. Transformants were selected on 300 mg/liter kanamycin, 100 mg/liter

ticarcillin/clavulanic acid (15:1, Duchefa Biochemie, Harlem, The Netherlands). Shoots were rooted on N13 medium (O'Connell et al., "Somatic Hybridization Between Lycopersicon-Esculentum and Lycopersicon-Pennellii," Theor. Appl. Genet., 70:1-12 (1985), which is hereby incorporated by reference in its entirety) before transfer to soil.

[0147] To determine whether Rf-PPR592 could restore fertility to rf/rf CMS lines, a 4.6-kb fragment carrying the entire coding region was introduced into the binary vector pGPTVKan. This fragment carries 2007 nt upstream of the start codon and 861 nt downstream of the stop codon. The pGPTVKan-4.6 kb Rf-PPR592 vector was transferred into A. tumefaciens strain LBA4404, which was used to transform a P. parodii rf/rf CMS line (Figure 4A) and a P. hybrida rf/rf CMS line (Figure 4C). More than two dozen independent transformants were obtained and grown to flowering. Fertile transformants were observed after transformation of both lines (Figures 4B and D). Among these were several fertile transformants carrying a single copy of the introduced Rf-PPR592 genomic DNA. Flowers of one of the P. parodii primary transformant plants were selfed, and a population of 40 T1 progeny was grown to flowering.

[0148] DNA extractions and Southern blotting were performed as described in Bentolila et al., "Locating the Petunia Rf Gene on a 650 kb DNA Fragment," Theor. Appl. Genet., 96:980-988 (1998), which is hereby incorporated by reference in its entirety. Floral bud protein was prepared for cell culture protein as described in Kohler et al., "The Green Fluorescent Protein as a Marker to Visualize Plant Mitochondria in vivo," Plant Journal, 11:613-621 (1997), which is hereby incorporated by reference in its entirety. After separation by SDS/PAGE (15%), immunoblots on Hybond-P poly(vinylidene difluoride) membranes (PVDF; Amersham Pharmacia, Picataway, NJ) were prepared as previously described (Reed et al., "High-Level Expression of a Synthetic Red-Shifted GFP Coding Region Incorporated into Transgenic Chloroplasts," Plant J., 27:257-2653 (2001), which is hereby incorporated by reference in its entirety) and probed with a 1:5000 dilution of the anti-PCF antibody (Nivison et al., "Sequencing, Processing, and Localization of the Petunia CMS-Associated Mitochondrial Protein," Plant J., 5:613-623 (1994), which is hereby incorporated by reference in its entirety).

[0149] DNA blot hybridization revealed that the fertile phenotype cosegregated with the Rf-PPR592 transgene (Figure 5A). The T1 progeny were also surveyed for the presence of the CMS-associated 19.5-kDa PCF protein. The 19.5-kDa protein was found to be decreased about 10-fold in fertile progeny restored by Rf-PPR592 relative to sterile progeny and the parental CMS line (Figure 5B). Thus, Rf-PPR592 was capable of restoring fertility by decreasing the amount of the PCF protein.

[0150] The cloning of a gene that can restore fertility to male-sterile *Petunia* lines will facilitate elucidation of the mechanism by which expression of the CMS-associated mitochondrial gene is suppressed. The reduced amount of the PCF protein could be due to a reduction in the abundance of one of the *Petunia* CMS-associated transcripts, which was reported previously (Pruitt et al., "Transcription of the *Petunia* Mitochondrial CMS-Associated *pcf* Locus in Male Sterile and Fertility-Restored Lines," Mol. Gen. Genet., 227:348-355 (1991), which is hereby incorporated by reference in its entirety), or to a translation defect that destabilizes the transcript. In yeast, mutation in a transcript-specific translation factor destabilizes the particular transcript with which the factor normally interacts (Poutre et al., "PET111, a Saccharomyces cerevisiae Nuclear Gene Required for Translation of the Mitochondrial mRNA Encoding Cytochrome C Oxidase Subunit II," Genetics, 115:637-647 (1987), which is hereby incorporated by reference in its entirety).

[0151] A number of fertility restorer genes in other species are known to alter transcript profiles and mitochondrial gene product accumulation (Moneger et al., "Nuclear Restoration of Cytoplasmic Male Sterility in Sunflower is Associated with the Tissue-Specific Regulation of a Novel Mitochondrial Gene," EMBO J., 13:8-17 (1994); Singh et al., "Nuclear Genes Associated With a Single Brassica CMS Restorer Locus Influence Transcripts of Three Different Mitochondrial Gene Regions," Genetics, 143:505-516 (1996); Dewey et al., "Novel Recombinations in the Maize Mitochondrial Genome Produce a Unique Transcriptional Unit in the Texas Male-Sterile Cytoplasm," Cell, 44:439-49 (1986); Wise et al., "Mitochondrial Transcript Processing and Restoration of Male Fertility in T-Cytoplasm Maize," J Hered, 90:380-385 (1999), which are hereby incorporated by reference in their entirety). In addition to the molecular phenotype of restoration, the *Petunia Rf* locus and *Rf* loci from other species may be similar in genomic organization (Li et al., "Restorer Genes

for Different Forms of *Brassica* Cytoplasmic Male Sterility Map to a Single Nuclear Locus That Modifies Transcripts of Several Mitochondrial Genes," Proc. Natl. Acad. Sci. USA, 95:10032-10037 (1998); Tang et al., "Cosegregation of Single Genes Associated with Fertility Restoration and Transcript Processing of Sorghum Mitochondrial *orf107* and *urf209*," Genetics, 150:383-391 (1998), which are hereby incorporated by reference in their entirety). The identification of *Petunia Rf* as a PPR family member suggests that searching for PPR motif genes near known restorer loci should be a useful strategy to identify candidate restorer genes in other species. Further studies of *Rf-PPR592* and other PPR motif-containing genes in plants, fungi, and animals will be required to determine whether the motif has a direct role in RNA-protein and/or protein-protein interactions.

Example 4 – Use of *Rf-PPR592* or its Homologs/Derivatives to Create Novel Floral Structures

[0152] In Petunia, recombination events near the Rf locus in standard sexual crosses resulted in plants with abnormal floral appearance. Moreover, a few of the initial transgenic plants transformed by Rf-PPR592 produced flowers with abnormal appearance. Furthermore, a number of transgenic plants transformed by Rf-PPR592 and Rf-PPR591 exhibit abnormalities in floral and vegetative structures. An example of abnormal flowers seen in some transgenic plants are shown in Figure 6.

Example 5 - Identification of a Rice Fertility Restorer Gene

[0153] The complete rice genome sequence, which has been deposited in EMBL/GenBank/DDBJ, was examined for genes similar to the petunia *Rf* gene, using BLASTP. The gene most similar to the petunia *Rf* locus was termed as *R*ice *h*omolog of *P*etunia *r*estorer 1 (*Rhpr1*). This gene is located very close to the rice *Rf4* marker C1261. There were a total of 10 PPR genes in the vicinity of this marker on rice chromosome 10, which were termed as *Rhpr1* to *Rhpr10* (SEQ ID NOs: 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38).

[0154] The most immediate usefulness of identification of the rice restorer gene is in marker-assisted selection. This facilitates introduction of the natural wild abortive-restorer *Rf4* gene, which can restore fertility to the wild abortive cytoplasm

by traditional crosses into elite breeding lines for use as a parent in a three-line breeding scheme. This use of the information does not involve genetically modified organisms and, therefore, can proceed without any of the attendant issues. Random screening has identified some molecular markers that are already being used to transfer *Rf* genes in certain nuclear backgrounds (Ichikawa et al., "A Rapid PCR-Aided Selection of a Rice Line Containing the *Rf-I* Gene Which is Involved in Restoration of the Cytoplasmic Male Sterility," Molecular Breeding, 3:195-202 (1997); Jing et al., "Mapping Fertility-Restoring Genes of Rice WA Cytoplasmic Male Sterility Using SSLP Markers," Bot. Bull. Acad. Sin., 42:167-171 (2001), which are hereby incorporated by reference in their entirety). Knowing the actual *Rf* gene sequence makes laborious screening for markers suitable between different breeding lines unnecessary.

[0155] The next possibility is to more rapidly transfer the *Rf4* gene into existing elite breeding lines by transformation rather than by sexual crosses. In such a strategy, the entire natural *Rf4* gene would be used to transform a rice line for the three-line hybrid rice production method.

[0156] Because the three-line method for hybrid rice production requires time-consuming breeding and labor, presently there are attempts to exploit temperature-sensitive male sterility mutants for a two-line method of hybrid seed production. The three-line method for hybrid rice production involves construction of three lines. Two lines are backcrossed repeatedly so that they contain the same nuclear genome. One contains the CMS cytoplasm ("CMS parent") and is male sterile while the other ("Fertile Maintainer") contains the normal cytoplasm but no restorer of fertility (*Rf*) alleles. By crossing the maintainer as male and the CMS line as female, seeds of the CMS line with a known nuclear background can be produced in large quantity. The third line is homozygous for one or more fertility restoration loci. Hybrid seed is produced by crossing the third line with the CMS parent. The nuclear genomes of the third line and the CMS line are selected by breeders to optimize heterosis and desirable characteristics for the region in which the hybrid rice will be grown.

[0157] Rice plants have been found that contain a mutant allele that encodes male sterility at high temperatures but fertility at low temperatures (Dong et al., "Molecular Mapping of a Rice Gene Conditioning Thermosensitive Genic Male Sterility Using AFLP, RFLP and SSR Techniques," Theor Appl Genet., 100:727-734

(2000), which is hereby incorporated by reference in its entirety). By growing the rice at high temperatures, it can be used as the sterile parent in a cross with an elite breeding line. The mutant rice can be propagated by selfing when grown at low temperatures. The use of this method in the field on large-scale has not been reported in the literature, so the feasibility of using a natural temperature-sensitive mutant is not known.

[0158] A cloned *Rf4* gene could also be used in a two-line method. In this scheme, the *Rf4* gene regulatory sequences would be engineered so that it could be turned on when desired. Then, both a CMS line and a maintainer line, which requires multiple crosses over a number of years to produce, are not needed. A single line, the CMS line containing the engineered *Rf4* gene, would serve both as CMS parent and as its own maintainer line (Figure 8). The CMS line would be propagated by selfing by turning on the *Rf4* gene. Without induction of the engineered *Rf4* gene, however, the line would be sterile and therefore could be used as a CMS parent.

[0159] Although the invention has been described in detail for the purpose of illustration, it is understood that such detail is solely for that purpose, and variations can be made therein by those skilled in the art without departing from the spirit and scope of the invention which is defined by the following claims.

WHAT IS CLAIMED:

1. An isolated nucleic acid molecule which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant, wherein the nucleic acid molecule: (1) encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41; (2) encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified by a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input; (3) hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C; or (4) has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

2. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

3. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ

ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

4. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

5. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

6. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

7. A isolated protein encoded by the nucleic acid molecule according to claim 1.

8. The isolated protein according to claim 7, wherein the protein has an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

9. The isolated protein according to claim 7, wherein the protein encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or

an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

10. The isolated protein according to claim 7, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

11. The isolated protein according to claim 7, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

12. The isolated protein according to claim 7, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

13. An isolated expression system comprising the nucleic acid molecule of claim 1.

14. The isolated expression system according to claim 13, wherein the nucleic acid molecule is in proper sense orientation.

15. An isolated host cell comprising the nucleic acid molecule of claim 1.

16. The isolated host cell according to claim 15, wherein the nucleic acid molecule is in an expression system.

17. The isolated host cell according to claim 15, wherein the host cell is a plant cell.

18. The isolated host cell according to claim 15, wherein the host cell is a bacterial cell.

19. A transgenic plant transformed with the nucleic acid molecule according to claim 1.

20. The transgenic plant according to claim 19, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

21. The transgenic plant according to claim 19, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

22. The transgenic plant according to claim 19, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

23. The transgenic plant according to claim 19, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID

NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

24. The transgenic plant according to claim 19, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

25. The transgenic plant according to claim 19, wherein the transgenic plant is a crop plant.

26. The transgenic plant according to claim 25, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

27. The transgenic plant according to claim 19, wherein the transgenic plant is an ornamental plant.

28. The transgenic plant according to claim 27, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

29. A transgenic plant seed transformed with the nucleic acid molecule according to claim 1.

30. The transgenic plant seed according to claim 29, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

31. The transgenic plant seed according to claim 29, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence

corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

32. The transgenic plant seed according to claim 29, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

33. The transgenic plant seed according to claim 29, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

34. The transgenic plant seed according to claim 29, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

35. The transgenic plant seed according to claim 29, wherein the transgenic plant is a crop plant.

36. The transgenic plant seed according to claim 35, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini,

cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

37. The transgenic plant seed according to claim 29, wherein the transgenic plant is an ornamental plant.

38. The transgenic plant seed according to claim 37, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

39. A method of restoring fertility to cytoplasmic male sterile plants comprising:

transforming a cytoplasmic male sterile plant with a nucleic acid molecule according to claim 1 under conditions effective to restore fertility to the cytoplasmic male sterile plant.

40. The method according to claim 39, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

41. The method according to claim 39, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

42. The method according to claim 39, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO:

40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

43. The method according to claim 39, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

44. The method according to claim 39, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

45. The method according to claim 39, wherein the plant is a crop plant.

46. The method according to claim 45, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

47. The method according to claim 39, wherein the plant is an ornamental plant.

48. The method according to claim 47, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

49. The method according to claim 39, wherein the plant has 2 or more copies of the nucleic acid molecule.

50. A method of identifying a candidate plant suitable for breeding with a cytoplasmic male sterile plant comprising:

analyzing the candidate plant for the presence, in its genome, of a nucleic acid molecule according to claim 1.

51. The method according to claim 50, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

52. The method according to claim 50, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

53. The method according to claim 50, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

54. The method according to claim 50, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

55. The method according to claim 50, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

56. The method according to claim 50, wherein the plant is a crop plant.

57. The method according to claim 56, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

58. The method according to claim 50, wherein the plant is an ornamental plant.

59. The method according to claim 58, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

60. A method of identifying a candidate gene restoring fertility in plants, said method comprising:

analyzing the candidate gene for the presence of a nucleic acid molecule according to claim 1.

61. The method according to claim 60, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

62. The method according to claim 60, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a

NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

63. The method according to claim 60, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

64. The method according to claim 60, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

65. The method according to claim 60, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

66. The method according to claim 60, wherein the plant is a crop plant.

67. The method according to claim 66, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

68. The method according to claim 60, wherein the plant is an ornamental plant.

69. The method according to claim 68, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

70. A method of producing hybrid plant seed comprising:

providing a cytoplasmic male sterile plant;

providing a second plant comprising a nucleic acid molecule according to claim 1; and

breeding the cytoplasmic male sterile plant and the second plant under conditions effective to produce hybrid progeny seed which yield fertile plants.

71. The method according to claim 70, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

72. The method according to claim 70, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

73. The method according to claim 70, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

74. The method according to claim 70, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

75. The method according to claim 70, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

76. The method according to claim 70, wherein the plants are crop plants.

77. The method according to claim 76, wherein the crop plants are selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

78. The method according to claim 70, wherein the plants are ornamental plants.

79. The method according to claim 78, wherein the ornamental plants are selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

80. The hybrid progeny seed produced by the method according to claim 70.

81. The hybrid progeny plants grown from the hybrid progeny seed produced by the method according to claim 70.

82. A method of producing plant seeds for an inbred line of plants comprising:

providing a cytoplasmic male sterile plant;

providing a second plant comprising a nucleic acid molecule according to claim 1;

breeding the cytoplasmic male sterile plant and the second plant under conditions effective to produce hybrid progeny seed which yield fertile plants;

producing hybrid fertile plants from the hybrid progeny seeds; and

backcrossing the hybrid fertile plants and the second plant to produce seed which yield inbred progeny plants.

83. The method according to claim 82, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

84. The method according to claim 82, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

85. The method according to claim 82, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

86. The method according to claim 82, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

87. The method according to claim 82, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

88. The method according to claim 82, wherein the plants are crop plants.

89. The method according to claim 88, wherein the crop plants are selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

90. The method according to claim 82, wherein the plants are ornamental plants.

91. The method according to claim 90, wherein the ornamental plants are selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

92. The seed which yield inbred progeny plants produced by the method according to claim 82.

93. The inbred progeny plants grown from the seed which yield inbred progeny plants produced by the method of claim 82.

94. A method of directing gene expression to plant mitochondria comprising:

transforming a plant with a chimeric nucleic acid molecule comprising a transgene operatively linked to a promoter or a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant, wherein the promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1 and the terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

95. The method according to claim 94, wherein the method is carried out with a promoter having a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1.

96. The method according to claim 94, wherein the method is carried out with a terminator having a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

97. The method according to claim 94, wherein the plant is a crop plant.

98. The method according to claim 97, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

99. The method according to claim 94, wherein the plant is an ornamental plant.

100. The method according to claim 99, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

101. A promoter from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant, wherein the promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1.

102. A terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant, wherein the terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

103. A nucleic acid construct comprising:

a promoter or a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant and

a nucleic acid heterologous to and operatively coupled to the promoter or the terminator, wherein the promoter has a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1 and the terminator has a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

104. A nucleic acid construct according to claim 103, wherein the construct is provided with a promoter from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant, said promoter having a nucleotide sequence of from nucleotide 1 to 1981 of SEQ ID NO: 1.

105. A nucleic acid construct according to claim 103, wherein the construct is provided with a terminator from a plant gene which restores fertility to cytoplasmic male sterile plants and modifies expression of toxic mitochondria proteins by the plant under conditions effective to direct expression of the transgene in the mitochondria of the transformed plant, said terminator having a nucleotide sequence of from nucleotide 3761 to 4593 of SEQ ID NO: 1.

106. An isolated expression system comprising the nucleic acid construct according to claim 103.

107. An isolated host cell comprising the nucleic acid construct according to claim 103.

108. A transgenic plant comprising the nucleic acid construct according to claim 103.

109. A transgenic plant seed comprising the nucleic acid construct according to claim 103.

110. A method of expressing a gene preferentially in roots of a plant comprising:

transforming a plant with a nucleic acid construct comprising: a promoter suitable for driving expression preferentially in roots having a nucleotide sequence of from 1 to 1388 of SEQ ID NO: 44; a nucleic acid heterologous to the promoter, wherein the promoter is operatively coupled 5' to the nucleic acid to induce transcription of the nucleic acid; and a terminator having a nucleotide sequence of from nucleotide 3168 to 4016 of SEQ ID NO: 44, wherein the terminator is operably coupled 3' to the nucleic acid.

111. The method according to claim 110, wherein the plant is a crop plant.

112. The method according to claim 111, wherein the crop plant is selected from the group consisting of alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

113. The method according to claim 111, wherein the plant is an ornamental plant.

114. The method according to claim 113, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

115. A method of altering plant floral morphology in ornamental plants comprising:

transforming an ornamental plant with a nucleic acid molecule according to claim 1.

116. The method according to claim 115, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

117. The method according to claim 115, wherein the nucleic acid encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

118. The method according to claim 115, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

119. The method according to claim 115, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

120. The method according to claim 115, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

121. The method according to claim 115, wherein the plant is an ornamental plant.

122. The method according to claim 121, wherein the ornamental plant is selected from the group consisting of *Arabidopsis thaliana*, *Saintpaulia*, petunia, pelargonium, poinsettia, chrysanthemum, carnation, and zinnia.

123. A method of producing plants with a cytoplasmic male sterile plant restoration system comprising:

transforming a first plant in its chloroplast genome with a nucleic acid which causes the plant to become male sterile;

transforming a second plant with a nucleic acid molecule according to claim 1 whose protein product is targeted to the chloroplast; and

crossing the first and second plants to produce progeny plants possessing a cytoplasmic male sterile plant restoration system.

124. The method according to claim 123, wherein the nucleic acid molecule encodes a protein having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, and 41.

125. The method according to claim 123, wherein the nucleic acid molecule encodes a protein comprising a motif having an amino acid sequence corresponding to any of SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input.

126. The method according to claim 123, wherein the nucleic acid molecule hybridizes to a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40 under stringent conditions of a hybridization buffer comprising 20% formamide in 0.9M saline/0.09M SSC buffer at a temperature of 42°C.

127. The method according to claim 123, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of from nucleotide 1982 to 3760 of SEQ ID NO: 1, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, and SEQ ID NO: 40.

128. The method according to claim 123, wherein the nucleic acid molecule is from petunia, *Arabidopsis thaliana*, or rice.

129. A method of producing plants with a cytoplasmic male sterile plant restoration system comprising:

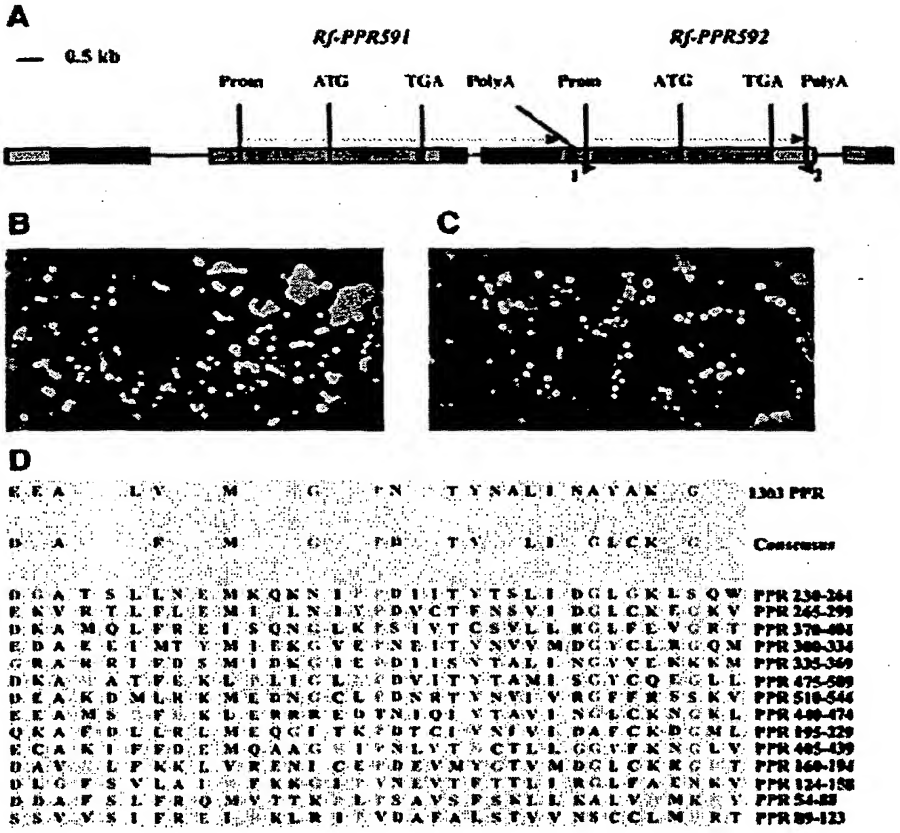
mutagenizing a first plant having a nucleic acid which encodes a protein comprising a motif having an amino acid sequence corresponding to any of

SEQ ID NOs: 3 to 18 or an amino acid sequence identified with a METAMEME software using the amino acid sequence of SEQ ID NO: 2 as input or an amino acid sequence identified as significantly similar to SEQ ID NO: 2 using a NCBI BLAST software (threshold= E less than or equal to 15) with SEQ ID NO: 2 as input;

crossing the mutagenized first plant with a wild-type plant having mitochondrial DNA polymorphisms compared to mitochondrial DNA in the mutagenized first plant to produce progeny plants; and

determining if the progeny plants are fertile, whereby fertile progeny plants can be used as a fertile maintainer line, wherein the mutagenized first plant, the fertile maintainer line, and a wild-type allele present in the first plant before mutagenesis comprises a new cytoplasmic male sterile plant restoration system.

130. An isolated nucleic acid sequence corresponding to SEQ ID NO: 42 or SEQ ID NO: 44.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PolyA
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ATG
TGA
PolyA
B
C
D

Figure 1

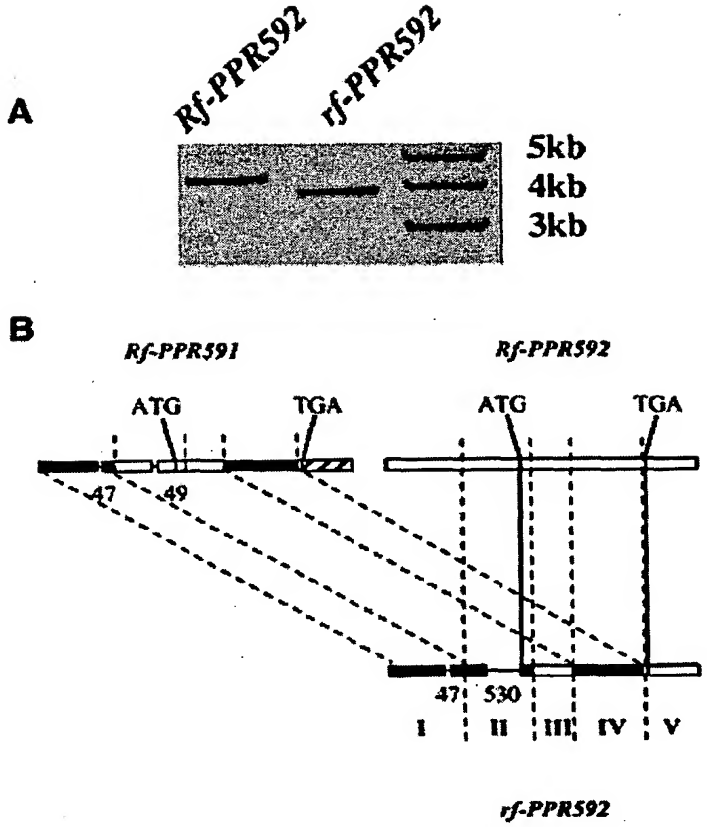
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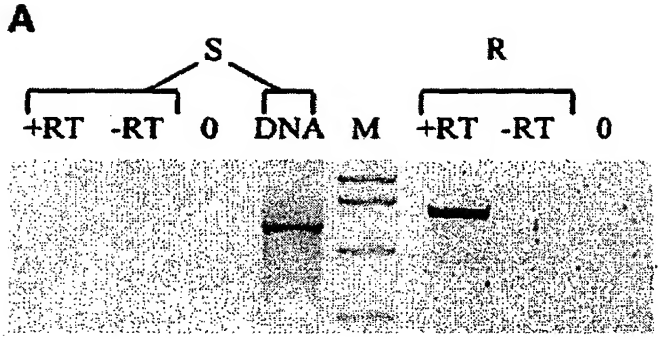
Figure 2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S
R
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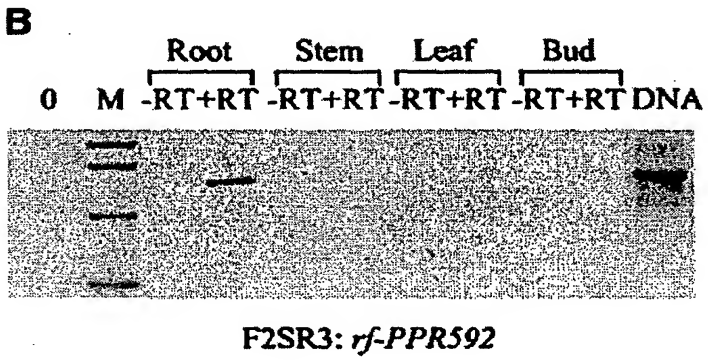

B
Root Stem Leaf Bud
0 M -RT+RT -RT+RT -RT+RT -RT+RT DNA
F2SR3: rf-PPR592

Figure 3

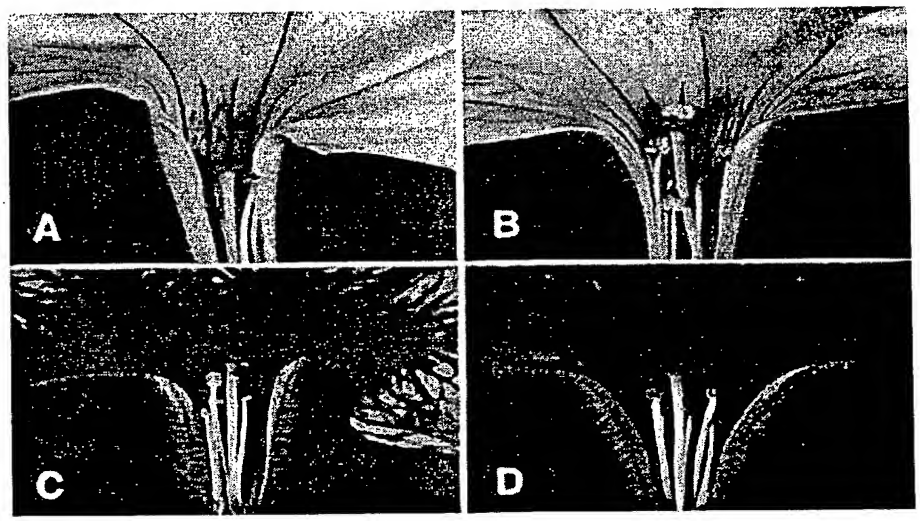


Figure 4

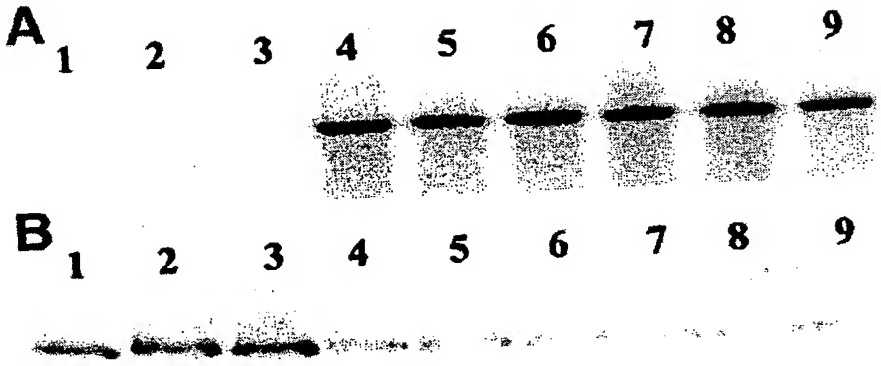


Figure 5

A. B.

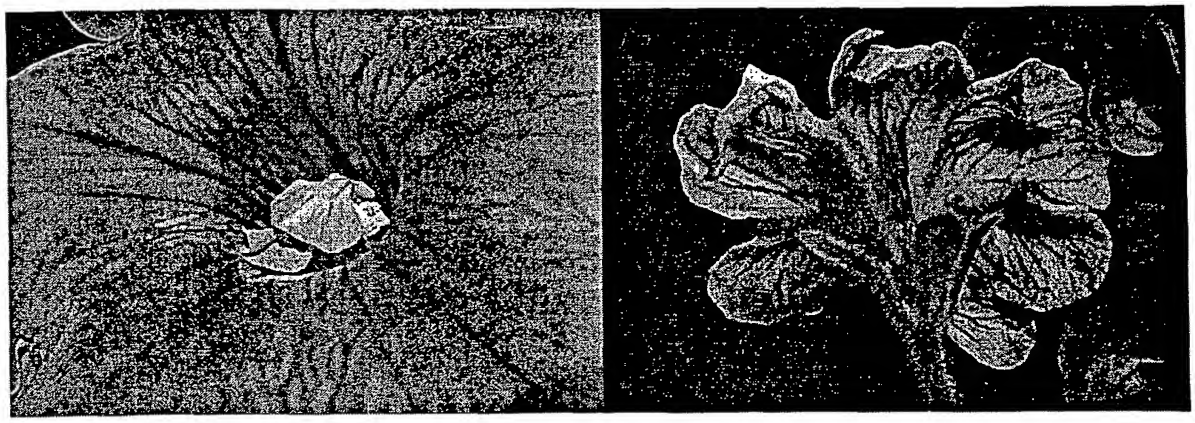
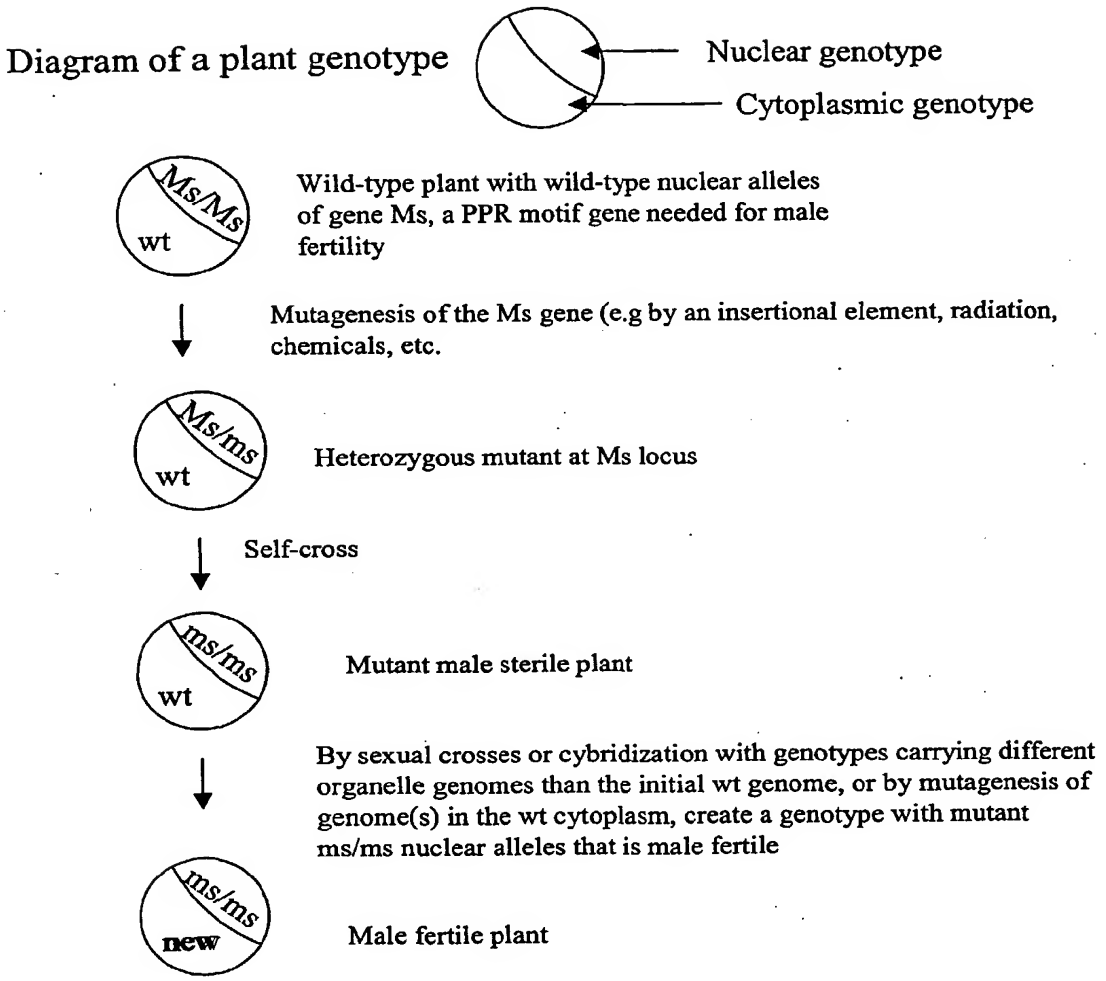


Figure 6



These genotypes are then utilized as a CMS/restorer system for hybrid seed production and breeding as follows:

Figure 7A

Examples illustrating how new lines can be used as a CMS/restorer system

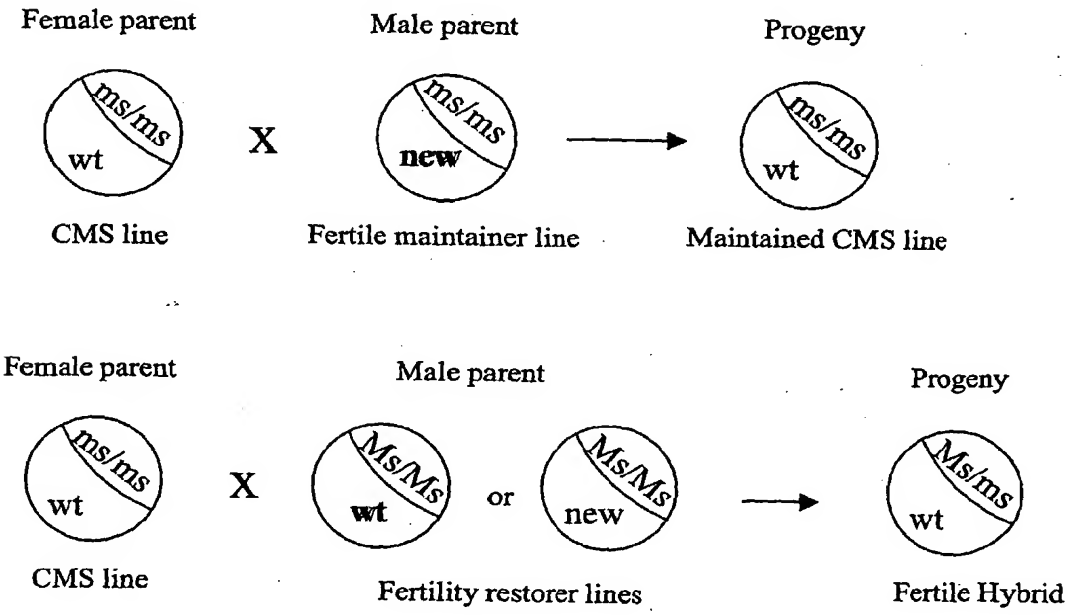


Figure 7B

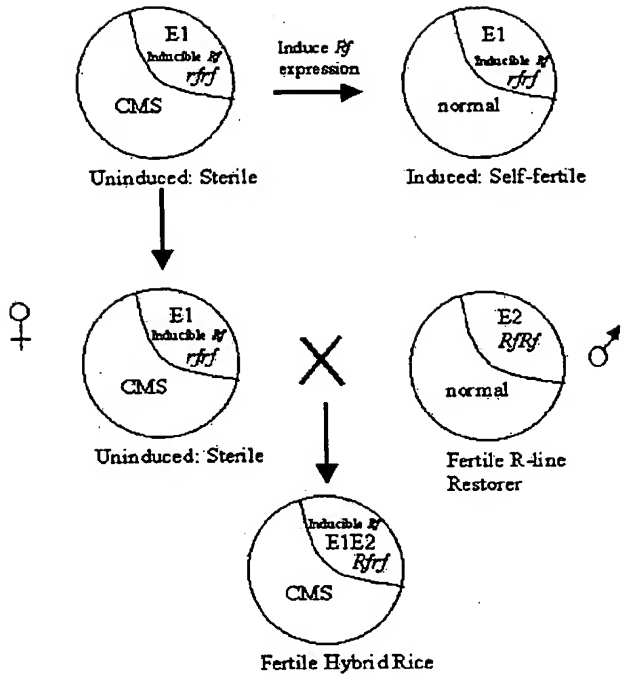

E1
Inducible Rf
rfrf
CMS
Induce Rf expression
E1
Inducible Rf
rfrf
normal
Uninduced: Sterile
Induced: Self-fertile
♀
E1
Inducible Rf
rfrf
CMS
Uninduced: Sterile
E2
RfRf
normal
♂
Fertile R-line Restorer
Inducible Rf
E1E2
Rfrf
CMS
Fertile Hybrid Rice

Figure 8

SEQUENCE LISTING

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<120> GENES FOR ALTERING MITOCHONDRIAL FUNCTION AND FOR HYBRID SEED PRODUCTION

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<212> PRT
<213> Petunia sp.

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Asn Val Lys Cys Leu Asp Asp Ala Phe Ser Leu Phe Arg Gln Met Val
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Thr Thr Lys Pro Leu Pro Ser Ala Val Ser Phe Ser Lys Leu Leu Lys
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Ala Leu Val His Met Lys His Tyr Ser Ser Val Val Ser Ile Phe Arg
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Glu Ile His Lys Leu Arg Ile Pro Val Asp Ala Phe Ala Leu Ser Thr
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Val Val Asn Ser Cys Cys Leu Met His Arg Thr Asp Leu Gly Phe Ser
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Val Leu Ala Ile His Phe Lys Lys Gly Ile Pro Tyr Asn Glu Val Thr
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Phe Thr Thr Leu Ile Arg Gly Leu Phe Ala Glu Asn Lys Val Lys Asp
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Ala Val His Leu Phe Lys Lys Leu Val Arg Glu Asn Ile Cys Glu Pro
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Asp Glu Val Met Tyr Gly Thr Val Met Asp Gly Leu Cys Lys Lys Gly

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His Thr Gln Lys Ala Phe Asp Leu Leu Arg Leu Met Glu Gln Gly Ile
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Thr Lys Pro Asp Thr Cys Ile Tyr Asn Ile Val Ile Asp Ala Phe Cys
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Lys Asp Gly Met Leu Asp Gly Ala Thr Ser Leu Leu Asn Glu Met Lys
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Gln Lys Asn Ile Pro Pro Asp Ile Ile Thr Tyr Thr Ser Leu Ile Asp
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Gly Leu Gly Lys Leu Ser Gln Trp Glu Lys Val Arg Thr Leu Phe Leu
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Glu Met Ile His Leu Asn Ile Tyr Pro Asp Val Cys Thr Phe Asn Ser
        275                 280                 285

Val Ile Asp Gly Leu Cys Lys Glu Gly Lys Val Glu Asp Ala Glu Glu
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Ile Met Thr Tyr Met Ile Glu Lys Gly Val Glu Pro Asn Glu Ile Thr
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Tyr Asn Val Val Met Asp Gly Tyr Cys Leu Arg Gly Gln Met Gly Arg
                325                 330                 335

Ala Arg Arg Ile Phe Asp Ser Met Ile Asp Lys Gly Ile Glu Pro Asp
            340                 345                 350

Ile Ile Ser Tyr Thr Ala Leu Ile Asn Gly Tyr Val Glu Lys Lys Lys
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Met Asp Lys Ala Met Gln Leu Phe Arg Glu Ile Ser Gln Asn Gly Leu
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Lys Pro Ser Ile Val Thr Cys Ser Val Leu Leu Arg Gly Leu Phe Glu
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Val Gly Arg Thr Glu Cys Ala Lys Ile Phe Phe Asp Glu Met Gln Ala
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Ala Gly His Ile Pro Asn Leu Tyr Thr His Cys Thr Leu Leu Gly Gly
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Tyr Phe Lys Asn Gly Leu Val Glu Glu Ala Met Ser His Phe His Lys
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465                 470                 475                 480

Phe Glu Lys Leu Pro Leu Ile Gly Leu His Pro Asp Val Ile Thr Tyr
                485                 490                 495

Thr Ala Met Ile Ser Gly Tyr Cys Gln Glu Gly Leu Leu Asp Glu Ala
            500                 505                 510

Lys Asp Met Leu Arg Lys Met Glu Asp Asn Gly Cys Leu Pro Asp Asn
        515                 520                 525

Arg Thr Tyr Asn Val Ile Val Arg Gly Phe Phe Arg Ser Ser Lys Val
    530                 535                 540

Ser Glu Met Lys Ala Phe Leu Lys Glu Ile Ala Gly Lys Ser Phe Ser
545                 550                 555                 560

Phe Glu Ala Ala Thr Val Glu Leu Leu Met Asp Ile Ile Ala Glu Asp
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Pro Ser Leu Leu Asn Met Ile Pro Glu Phe His Arg Asp Asn Lys Lys
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<220>
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<213> Petunia sp.

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Pro Ser Ala Val Ser Phe Ser Lys Leu Leu Lys Ala Leu Val His Met
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Lys His Tyr
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<212> PRT
<213> Petunia sp.

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His Arg Thr
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<212> PRT
<213> Petunia sp.

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Asn Lys Val
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Gly His Thr
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<213> Petunia sp.

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Pro Asp Thr Cys Ile Tyr Asn Ile Val Ile Asp Ala Phe Cys Lys Asp
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Gly Met Leu
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<210> 10
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<213> Petunia sp.

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Pro Asp Ile Ile Thr Tyr Thr Ser Leu Ile Asp Gly Leu Gly Lys Leu
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Ser Gln Trp
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<212> PRT
<213> Petunia sp.

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Gly Lys Val
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<212> PRT
<213> Petunia sp.

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Gly Gln Met
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<210> 13
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<212> PRT
<213> Petunia sp.

<400> 13
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Pro Asp Ile Ile Ser Tyr Thr Ala Leu Ile Asn Gly Tyr Val Glu Lys
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Lys Lys Met
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<212> PRT
<213> Petunia sp.

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Gly Arg Thr
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<213> Petunia sp.

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Gly Leu Val
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<212> PRT
<213> Petunia sp.

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Gly Lys Leu
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<211> 35
<212> PRT
<213> Petunia sp.

<400> 17
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Pro Asp Val Ile Thr Tyr Thr Ala Met Ile Ser Gly Tyr Cys Gln Glu
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Gly Leu Leu
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<210> 18
<211> 35
<212> PRT
<213> Petunia sp.

<400> 18
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Ser Lys Val
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35 40 45

Arg Gly Arg Gly Ala Ser Ile Tyr Gly Leu Asn Arg Ala Leu Ala Asp
50 55 60

Val Ala Arg His Ser Pro Ala Ala Ala Val Ser Arg Tyr Asn Arg Met
65 70 75 80

Ala Arg Ala Gly Ala Gly Lys Val Thr Pro Thr Val His Thr Tyr Ala
85 90 95

Ile Leu Ile Gly Cys Cys Cys Arg Ala Gly Arg Leu Asp Leu Gly Phe
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Ala Ala Leu Gly Asn Val Val Lys Lys Gly Phe Arg Val Asp Ala Ile
115 120 125

Thr Phe Thr Pro Leu Leu Lys Gly Leu Cys Ala Asp Lys Arg Thr Ser
130 135 140

Asp Ala Met Asp Ile Val Leu Arg Arg Met Thr Glu Leu Gly Cys Ile
145 150 155 160

Pro Asp Val Phe Ser Tyr Asn Asn Leu Leu Lys Gly Leu Cys Asp Glu
165 170 175

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Arg Gly Gly Gly Ser Pro Pro Asp Val Val Ser Tyr Asn Thr Val Leu
        195                 200                 205

Asn Gly Phe Phe Lys Glu Gly Asp Ser Asp Lys Ala Tyr Ser Thr Tyr
    210                 215                 220

His Glu Met Leu Asp Arg Gly Ile Leu Pro Asp Val Val Thr Tyr Ser
225                 230                 235                 240

Ser Ile Ile Ala Ala Leu Cys Lys Ala Gln Ala Met Asp Lys Ala Met
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Glu Val Leu Asn Thr Met Val Lys Asn Gly Val Met Pro Asp Cys Met
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Thr Tyr Asn Ser Ile Leu His Gly Tyr Cys Ser Ser Gly Gln Pro Lys
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Glu Ala Ile Gly Thr Leu Lys Lys Met Arg Ser Asp Gly Val Glu Pro
    290                 295                 300

Asn Val Val Thr Tyr Ser Ser Leu Met Asn Tyr Leu Cys Lys Asn Gly
305                 310                 315                 320

Arg Ser Thr Glu Ala Arg Lys Ile Phe Asp Ser Met Thr Lys Arg Gly
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Leu Glu Pro Asp Ile Ala Thr Tyr Arg Thr Leu Leu Gln Gly Tyr Ala
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Thr Lys Gly Ala Leu Val Glu Met His Ala Leu Leu Asp Leu Met Val
        355                 360                 365

Arg Asn Gly Ile Gln Pro Asp His His Val Phe Asn Ile Leu Ile Cys
    370                 375                 380

Ala Tyr Ala Lys Gln Glu Lys Val Asp Gln Ala Met Leu Val Phe Ser
385                 390                 395                 400

Lys Met Arg Gln His Gly Leu Asn Pro Asn Val Val Cys Tyr Gly Thr
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Val Ile Asp Val Leu Cys Lys Ser Gly Ser Val Asp Asp Ala Met Leu
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Tyr Thr Ser Leu Ile His Gly Leu Cys Thr Cys Asp Lys Trp Asp Lys
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Thr Ile Phe Phe Asn Ser Ile Ile Asp Ser His Cys Lys Glu Gly Arg
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Lys Pro Asp Ile Ile Thr Tyr Asn Thr Leu Ile Asp Gly Cys Cys Leu
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Ala Gly Lys Met Asp Glu Ala Thr Lys Leu Leu Ala Ser Met Val Ser
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Val Gly Val Lys Pro Asp Ile Val Thr Tyr Gly Thr Leu Ile Asn Gly
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Tyr Cys Arg Val Ser Arg Met Asp Asp Ala Leu Ala Leu Phe Lys Glu
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Met Val Ser Ser Gly Val Ser Pro Asn Ile Ile Thr Tyr Asn Ile Ile
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Leu Gln Gly Leu Phe His Thr Arg Arg Thr Ala Ala Ala Lys Glu Leu
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Tyr Val Ser Ile Thr Lys Ser Gly Thr Gln Leu Glu Leu Ser Thr Tyr
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Asn Ile Ile Leu His Gly Leu Cys Lys Asn Asn Leu Thr Asp Glu Ala
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Leu Arg Met Phe Gln Asn Leu Cys Leu Thr Asp Leu Gln Leu Glu Thr
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Arg Thr Phe Asn Ile Met Ile Gly Ala Leu Leu Lys Cys Gly Arg Met
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Asp Glu Ala Lys Asp Leu Phe Ala Ala His Ser Ala Asn Gly Leu Val
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Gly Ser Leu Glu Glu Leu Asp Asp Leu Phe Leu Ser Met Glu Glu Asn
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Gly Cys Ser Ala Asp Ser Arg Met Leu Asn Ser Ile Val Arg Lys Leu
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Leu Gln Arg Gly Asp Ile Thr Arg Ala Gly Thr Tyr Leu Phe Met Ile
            740                 745                 750

Asp Glu Lys His Phe Ser Leu Glu Ala Ser Thr Ala Ser Phe Leu Leu
        755                 760                 765

Glu Ser Ser Pro Ile Val Trp Glu Gln Ile Ser Arg Ile Ser His Leu
    770                 775                 780

Ser Val Asn Leu Lys Leu Ile Lys Gln Pro Lys Cys Thr Cys Glu Leu
785                 790                 795                 800

Gly Pro Lys Trp Ser Gln Asn Leu Pro Lys Pro Gly Thr Asn Ser Val
                805                 810                 815

Gly Ser Val Ala Gln Phe His Leu Ser Arg Gly Gly Tyr Arg Ala Tyr
            820                 825                 830

Arg Gly Gly Thr Thr Val Thr Ala Leu Pro Gln Gly Asp Gly Asn Pro
        835                 840                 845

Gly Pro Asn Asp Lys Val Asn Pro Gly Arg Thr Asn Leu Ala Gln Asn
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35 40 45

Gly Arg Gly Ala Ser Ile Tyr Gly Leu Asn Cys Ala Leu Ala Asp Val
50 55 60

Ala Arg His Ser Pro Ala Ala Ala Val Ser Arg Tyr Asn Arg Met Ala
65 70 75 80

Arg Ala Gly Ala Asp Glu Val Thr Pro Asn Leu Cys Thr Tyr Gly Ile
85 90 95

Leu Ile Gly Ser Cys Cys Cys Ala Gly Arg Leu Asp Leu Gly Phe Ala
100 105 110

Ala Leu Gly Asn Val Ile Lys Lys Gly Phe Arg Val Asp Ala Ile Ala
115 120 125

Phe Thr Pro Leu Leu Lys Gly Leu Cys Ala Asp Lys Arg Thr Ser Asp
130 135 140

Ala Met Asp Ile Val Leu Arg Arg Met Thr Gln Leu Gly Cys Ile Pro
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Asn Val Phe Ser Tyr Asn Ile Leu Leu Lys Gly Leu Cys Asp Glu Asn

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Lys Ile Ser Arg Met Glu Asp Ala Leu Val Leu Phe Arg Glu Met Glu
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Ser Ser Gly Val Ser Pro Asp Ile Ile Thr Tyr Asn Ile Ile Leu Gln
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Met Phe Gln Asn Leu Cys Leu Thr Asp Leu Gln Leu Glu Thr Arg Thr
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Phe Asn Ile Met Ile Gly Ala Leu Leu Lys Val Gly Arg Asn Asp Glu
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Ala Lys Asp Leu Phe Ala Ala Leu Ser Ala Asn Gly Leu Val Pro Asp
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Thr Ala Asn Ser Arg Met Leu Asn Ser Ile Val Arg Lys Leu Leu Gln
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Arg Gly Asp Ile Thr Arg Ala Gly Thr Tyr Leu Phe Met Ile Asp Glu
740 745 750

Lys His Phe Ser Leu Glu Ala Ser Thr Ala Scr Leu Phe Leu Asp Leu
755 760 765

Leu Ser Gly Gly Lys Tyr Gln Glu Tyr His Ser Cys Ile Arg Gly Gly
770 775 780

Ile Phe Ser Leu Cys Val Asn Ser Glu Val Gln Glu Asn His Leu Leu
785 790 795 800

Asp Ser Glu Ser Gly Val His Phe Leu Leu Lys Leu Leu Asn Pro Pro
805 810 815

Val Asn Leu Val Asp Ser Lys Ala Pro Ser Ile Gly Ser Lys Leu Leu
820 825 830

Gly Ile Ser Lys Val Gln Met Leu Asn Gly Ser Asn Lys Asp Ser Asp
835 840 845

Cys Ile Ser Glu Glu Ile Leu Ser Lys Val Glu Glu Ile Leu Leu Ser
850 855 860

Cys Gln Val Ile Lys Ser Leu Asp Lys Asp Asp Lys Lys Thr Thr Arg
865 870 875 880

Pro Glu Leu Cys Pro Lys Trp Leu Ala Leu Leu Thr Met Glu Asn Ala
885 890 895

Cys Leu Ser Ala Val Ser Val Glu Glu Thr Ser Asp Thr Val Ser Arg
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Val Gly Gly Asn Phe Lys Glu Thr Leu Arg Glu Met Gly Gly Leu Asp
915 920 925

Ser Ile Phe Asp Val Met Val Asp Phe His Ser Thr Leu Glu Asn Leu

930 935 940

Ile Lys Asp Thr Ser Thr Ser Ala Leu Asp Arg Asn Glu Gly Thr Ser
945 950 955 960

Leu Gln Ser Ala Ala Leu Leu Leu Lys Cys Leu Lys Ile Leu Glu Asn
965 970 975

Ala Ile Phe Leu Ser Asp Asp Asn Lys Thr His Leu Leu Asn Met Ser
980 985 990

Arg Lys Leu Asn Pro Lys Arg Ser Leu Leu Ser Phe Val Gly Val Ile
995 1000 1005

Ile Asn Thr Ile Glu Leu Leu Ser Ala Leu Ser Ile Leu Gln Asn Ser
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Ser Val Val Ser Ser Ser Thr Tyr Pro Lys Ser Ser Lys Val Ser Gln
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Gln Ser Tyr Ser Val Val Met Ala Gly Gly Asp Arg Gly Arg Gly Val
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Glu Cys His Pro His Gln Gly Val Ser Ala Ala Leu Leu Arg Pro Gly
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Pro Gln Ala Leu Ala Ala Ser Trp Arg Arg Arg Glu Thr Val Val Arg
1075 1080 1085

Ser Asp Phe Ala Ala Gly Gly Val Ala Thr Met Gly Asp Ser Pro Gln
1090 1095 1100

Ala Leu Ser Asp Arg Leu Cys Gly Ser Ala Thr Lys Val Trp Arg Gly
1105 1110 1115 1120

Gly Ala Glu Trp Thr Ala Glu Ala Phe Ala Arg Asn Gly Ala Ala Gly
1125 1130 1135

Pro Ser Gln Ser Arg Leu Pro Val Thr Arg Asn Arg Ala Gln His Tyr
1140 1145 1150

Ile Ala Lys Ile Trp Ala Thr Leu Thr Ile Ser Met Phe Tyr Lys Leu
1155 1160 1165

Asp Val Glu Gly Met Glu Asn Leu Pro Pro Asn Ser Ser Pro Ala Ile
1170 1175 1180

Tyr Val Ala Asn His Gln Ser Phe Leu Asp Ile Tyr Thr Leu Leu Thr

1185 1190 1195 1200

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Asp Ala Arg His Val Phe Asp Glu Leu Leu Arg Arg Gly Arg Gly Ala
35 40 45

Ser Ile Tyr Gly Leu Asn Arg Ala Leu Ala Asp Val Ala Arg His Ser
50 55 60

Pro Ala Ala Ala Val Ser Arg Tyr Asn Arg Met Ala Arg Ala Gly Ala
65 70 75 80

Asp Glu Val Thr Pro Asp Leu Cys Thr Tyr Gly Ile Leu Ile Gly Cys
85 90 95

Cys Cys Arg Ala Gly Arg Leu Asp Leu Gly Phe Ala Ala Leu Gly Asn
100 105 110

Val Ile Lys Lys Gly Phe Arg Val Glu Ala Ile Thr Phe Thr Pro Leu
115 120 125

Leu Lys Gly Leu Cys Ala Asp Lys Arg Thr Ser Asp Ala Met Asp Ile

130 135 140

Val Leu Arg Arg Met Thr Glu Leu Gly Cys Ile Pro Asn Val Phe Ser
145 150 155 160

Tyr Asn Asn Leu Leu Asn Gly Leu Cys Asp Glu Asn Arg Ser Gln Glu
165 170 175

Ala Leu Glu Leu Leu His Met Met Ala Asp Asp Arg Gly Gly Gly Ser
180 185 190

Pro Pro Asp Val Val Ser Tyr Thr Thr Val Ile Asn Gly Phe Phe Lys
195 200 205

Glu Gly Asp Ser Asp Lys Ala Tyr Ser Thr Tyr His Glu Met Leu Asp
210 215 220

Arg Gly Ile Leu Pro Asp Val Val Thr Tyr Ser Ser Ile Ile Ala Ala
225 230 235 240

Leu Cys Lys Gly Gln Ala Met Asp Lys Pro Trp Ser His Cys Lys Glu
245 250 255

Gly Arg Val Ile Glu Ser Glu Lys Leu Phe Asp Leu Met Val Arg Ile
260 265 270

Gly Val Lys Pro Asp Ile Ile Thr Tyr Ser Thr Leu Ile Asp Gly Tyr
275 280 285

Cys Leu Ala Gly Lys Met Asp Glu Ala Met Lys Leu Leu Ser Gly Met
290 295 300

Val Ser Val Gly Leu Lys Pro Asn Thr Val Thr Tyr Ser Thr Leu Ile
305 310 315 320

Asn Gly Tyr Cys Lys Ile Ser Arg Met Glu Asp Ala Leu Val Leu Phe
325 330 335

Lys Glu Met Glu Ser Ser Gly Val Ser Pro Asp Ile Ile Thr Tyr Asn
340 345 350

Ile Ile Leu Gln Gly Leu Phe Gln Thr Arg Arg Thr Ala Ala Ala Lys
355 360 365

Glu Leu Tyr Val Arg Ile Thr Glu Ser Gly Thr Gln Ile Glu Leu Ser
370 375 380

Thr Tyr Asn Ile Ile Leu His Gly Leu Cys Lys Asn Lys Leu Thr Asp

385 390 395 400

Asp Ala Leu Gln Met Phe Gln Asn Leu Cys Leu Met Asp Leu Lys Leu
405 410 415

Glu Ala Arg Thr Phe Asn Ile Met Ile Asp Ala Leu Leu Lys Val Gly
420 425 430

Arg Asn Asp Glu Ala Lys Asp Leu Phe Val Ala Phe Ser Ser Asn Gly
435 440 445

Leu Val Pro Asn Tyr Trp Thr Tyr Arg Leu Met Ala Glu Asn Ile Ile
450 455 460

Gly Gln Gly Leu Leu Glu Glu Leu Asp Gln Leu Phe Leu Ser Met Glu
465 470 475 480

Asp Asn Gly Cys Thr Val Asp Ser Gly Met Leu Asn Phe Ile Val Arg
485 490 495

Glu Leu Leu Gln Arg Gly Val Val Val Val Val Ser Gly Glu Ser Ala
500 505 510

Thr Thr Pro Pro Pro Thr Leu Lys Ile Leu Thr Cys Gly Ile Thr Val
515 520 525

Asn Pro Phe Ser Lys Thr Cys Gly Ile Thr Val Asn Pro Phe Ser Lys
530 535 540

Pro Ile Val Gln Thr Gly Ala Cys Gly Gln Val Lys Glu Val Gly Lys
545 550 555 560

Asn Ala Ser Glu Glu Arg Leu Ile Val Val Ser Ser Gln Glu Ile Pro
565 570 575

Asp Asp Pro Val Ser Pro Thr Ile Glu Ala Leu Ile Leu Leu His Ser
580 585 590

Lys Ala Ser Thr Leu Ala Glu Asn His Gln Leu Thr Thr Arg Leu Val
595 600 605

Val Pro Ser Asn Lys Val Gly Cys Ile Leu Gly Glu Gly Gly Lys Val
610 615 620

Ile Thr Glu Met Arg Arg Arg Thr Gly Ala Glu Ile Arg Val Tyr Ser
625 630 635 640

Lys Ala Asp Lys Pro Lys Tyr Leu Ser Phe Asp Glu Glu Leu Val Gln

645 650 655

His Ile Ser Leu Ile Leu Val Asp Arg His Ala Gly Arg Ala His Leu
660 665 670

Leu Ser His Gln Leu Leu Thr Ala Ile Tyr Val Leu Val Leu Asn Arg
675 680 685

Ser Ile Val Val Ala Glu Val Lys Asn Asn His Gly Thr Ala Ala Cys
690 695 700

Trp Ala Leu Ala Ala Ile Ser Tyr Asn Arg Thr Asn Phe Ser Asp Leu
705 710 715 720

Leu Val Ser His Trp Phe Ile Ile Lys Ala Ser Val Phe Ser Phe Thr
725 730 735

Leu Gly Leu Gln Asn Leu Arg Thr Gly Pro Ala His Asp Pro Tyr Thr
740 745 750

Val Tyr Pro Val Glu Tyr Phe Ser Lys Arg Glu Tyr Pro Ser Gly Ser
755 760 765

Ser Lys Val Ala Pro Ser Ala Ser Tyr Glu Arg Tyr Ala Ala Thr Thr
770 775 780

Arg Leu Pro Asn Gly Glu Leu Pro Ser Ser Ile Ser Pro Gly Ala Asp
785 790 795 800

Tyr Met Ser Cys Arg Ser Tyr Leu Asp Gln Val Pro Thr Asp Arg Tyr
805 810 815

Ser Asn Arg Val Thr Leu Gln Leu Gly Leu Ser Arg Ala Gly Asn Ser
820 825 830

Asn Val Gln Gln Leu Gly Ile Thr Arg Ala Gly Asn Ser Asn Ala Tyr
835 840 845

Asp Tyr Thr Glu Ala Ala Glu Gln Ile His Gly Arg Glu Asp Tyr Arg
850 855 860

Arg Leu Ser Gly Leu Thr Gly Tyr Pro Gly Gly Ser Ser Asn Cys Gly
865 870 875 880

Phe Gln Ile Val Asn Trp Ser Leu Ser Leu Val Leu Val Ile Ser Gly
885 890 895

Ala Arg Val Lys Leu His Glu Ala His Pro Gly Ser Ser Glu Ser Ile

900 905 910

Val Glu Ile Gln Gly Ile Pro Asp Gln Val Lys Ala Ala Gln Ser Leu
915 920 925

Leu Gln Gly Phe Ile Gly Ala Ser Ser Asn Ser Arg Gln Ala Pro Gln
930 935 940

Ser Ser Arg Met Ala His Tyr Phe
945 950

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<400> 27

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Leu Leu His Leu Leu Leu Arg Thr Ala Pro Pro Pro Pro Leu Pro Asp
        35                  40                  45

Leu Val Ser Leu Ala Arg Trp Ser Arg Ala His Phe Arg Ala Pro Leu
    50                  55                  60

Pro Leu Arg Leu His Gly Leu Leu Leu Ala Arg Leu Ala Ser Lys Gly
65                  70                  75                  80

Leu Tyr Pro Leu Leu Arg Ser Glu Leu His Val Leu Ala Ala Ala Arg
                85                  90                  95

Leu His Ser Pro Ala Ser Ile Leu Arg Ala Leu Pro Ser Pro Ser Ala
            100                 105                 110

Ser Ala Ser Ala Ser Thr Pro Leu Ile Ala Asp Met Leu Val Leu Ala
        115                 120                 125

Leu Ala Arg Ala Ser Gln Pro Leu Arg Ala Tyr Asp Ala Phe Leu Leu
    130                 135                 140

Ala Gly Glu Ser His Pro Arg His Arg Pro Ser Thr Ser Ser Val Asn
145                 150                 155                 160

Ala Leu Leu Ala Gly Leu Val Gly Ala Lys Arg Val Asp Leu Ala Glu
                165                 170                 175

Lys Ala Phe Arg Ser Ala Leu Arg Arg Arg Val Ser Pro Asp Ile Tyr
            180                 185                 190

Thr Phe Asn Thr Val Ile Ser Gly Leu Cys Arg Ile Gly Gln Leu Arg
        195                 200                 205

Lys Ala Gly Asp Val Ala Lys Asp Ile Lys Ala Trp Gly Leu Ala Pro
    210                 215                 220
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Ser Val Ala Thr Tyr Asn Ser Leu Ile Asp Gly Tyr Cys Lys Lys Gly
225                 230                 235                 240

Gly Ala Gly Asn Met Tyr His Val Asp Met Leu Leu Lys Glu Met Val
                245                 250                 255

Glu Ala Gly Ile Ser Pro Thr Ala Val Thr Phe Gly Val Leu Ile Asn
            260                 265                 270

Gly Tyr Cys Lys Asn Ser Asn Thr Ala Ala Ala Val Arg Val Phe Glu
        275                 280                 285

Glu Met Lys Gln Gln Gly Ile Ala Ala Ser Val Val Thr Tyr Asn Ser
    290                 295                 300

Leu Ile Ser Gly Leu Cys Ser Glu Gly Lys Val Glu Glu Gly Val Lys
305                 310                 315                 320

Leu Met Glu Glu Met Glu Asp Leu Gly Leu Ser Pro Asn Glu Ile Thr
                325                 330                 335

Phe Gly Cys Val Leu Lys Gly Phe Cys Lys Lys Gly Met Met Ala Asp
            340                 345                 350

Ala Asn Asp Trp Ile Asp Gly Met Thr Glu Arg Asn Val Glu Pro Asp
        355                 360                 365

Val Val Ile Tyr Asn Ile Leu Ile Asp Val Tyr Arg Arg Leu Gly Lys
    370                 375                 380

Met Glu Asp Ala Met Ala Val Lys Glu Ala Met Ala Lys Lys Gly Ile
385                 390                 395                 400

Ser Pro Asn Val Thr Thr Tyr Asn Cys Leu Ile Thr Gly Phe Ser Arg
                405                 410                 415

Ser Gly Asp Trp Arg Ser Ala Ser Gly Leu Leu Asp Glu Met Lys Glu
            420                 425                 430

Lys Gly Ile Glu Ala Asp Val Val Thr Tyr Asn Val Leu Ile Gly Ala
        435                 440                 445

Leu Cys Cys Lys Gly Glu Val Arg Lys Ala Val Lys Leu Leu Asp Glu
    450                 455                 460

Met Ser Glu Val Gly Leu Glu Pro Asn His Leu Thr Tyr Asn Thr Ile
465                 470                 475                 480
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Ile Gln Gly Phe Cys Asp Lys Gly Asn Ile Lys Ser Ala Tyr Glu Ile
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Arg Thr Arg Met Glu Lys Cys Arg Lys Arg Ala Asn Val Val Thr Tyr
            500                 505                 510

Asn Val Phe Ile Lys Tyr Phe Cys Gln Ile Gly Lys Met Asp Glu Ala
        515                 520                 525

Asn Asp Leu Leu Asn Glu Met Leu Asp Lys Cys Leu Val Pro Asn Gly
    530                 535                 540

Ile Thr Tyr Glu Thr Ile Lys Glu Gly Met Met Glu Lys Gly Tyr Thr
545                 550                 555                 560

Pro Asp Ile Arg Gly Cys Thr Val Ser Gln Ala Ser Glu Asn Pro Ala
                565                 570                 575

Ser Ser
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<212> DNA
<213> Oryza sativa

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<210> 29
<211> 454
<212> PRT
<213> Oryza sativa

<400> 29

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             20                  25                  30

Thr Tyr His Glu Met Leu Asp Arg Arg Val Ser Pro Asp Ala Val Thr
         35                  40                  45

Tyr Asn Ser Ile Ile Ala Ala Leu Ser Lys Ala Gln Ala Met Asp Arg
     50                  55                  60

Ala Met Glu Val Leu Thr Val Met Val Met Pro Asn Cys Phe Thr Tyr
 65                  70                  75                  80

Asn Ser Ile Met His Gly Tyr Cys Ser Ser Gly Gln Ser Glu Lys Ala
                 85                  90                  95

Ile Gly Ile Phe Arg Lys Met Cys Ser Asp Gly Ile Glu Pro Asp Val
            100                 105                 110

Val Thr Tyr Asn Ser Leu Met Asp Tyr Leu Cys Lys Asn Gly Lys Cys
        115                 120                 125

Thr Glu Ala Arg Lys Ile Phe Asp Ser Met Val Lys Arg Gly Leu Lys
    130                 135                 140

Pro Asp Ile Thr Thr Tyr Gly Thr Leu Leu His Gly Tyr Ala Ser Lys
145                 150                 155                 160

Gly Ala Leu Val Glu Met His Asp Leu Leu Ala Leu Met Val Gln Asn
                165                 170                 175

Gly Met Gln Leu Asp His His Val Phe Asn Ile Leu Ile Cys Ala Tyr
            180                 185                 190
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Thr Lys Gln Glu Lys Val Asp Glu Val Val Leu Val Phe Ser Lys Met
        195                 200                 205

Arg Gln Gln Gly Leu Thr Pro Asn Ala Val Asn Tyr Arg Thr Val Ile
    210                 215                 220

Asp Gly Leu Cys Lys Leu Gly Arg Leu Asp Asp Ala Met Leu Asn Phe
225                 230                 235                 240

Glu Gln Met Ile Asp Lys Gly Leu Thr Pro Asn Val Val Val Tyr Thr
                245                 250                 255

Ser Leu Ile His Ala Leu Cys Thr Tyr Asp Lys Trp Glu Lys Ala Glu
            260                 265                 270

Glu Leu Ile Phe Glu Ile Leu Asp Gln Gly Ile Asn Pro Asn Ile Val
        275                 280                 285

Phe Phe Asn Thr Ile Leu Asp Ser Leu Cys Lys Glu Gly Arg Val Ile
    290                 295                 300

Glu Ser Lys Lys Leu Phe Asp Leu Leu Gly His Ile Gly Val Asn Pro
305                 310                 315                 320

Asp Val Ile Thr Tyr Ser Thr Leu Ile Asp Gly Tyr Cys Leu Ala Gly
                325                 330                 335

Lys Met Asp Gly Ala Met Lys Leu Leu Thr Gly Met Val Ser Val Gly
            340                 345                 350

Leu Lys Pro Asp Ser Val Thr Tyr Ser Thr Leu Ile Asn Gly Tyr Cys
        355                 360                 365

Lys Ile Asn Arg Met Glu Asp Ala Leu Ala Leu Phe Lys Glu Met Glu
    370                 375                 380

Ser Asn Gly Val Asn Pro Asp Ile Ile Thr Tyr Asn Ile Ile Leu His
385                 390                 395                 400

Gly Leu Phe Arg Thr Arg Arg Thr Ala Ala Ala Lys Glu Leu Tyr Ala
                405                 410                 415

Arg Ile Thr Glu Ser Gly Thr Gln Leu Glu Leu Ser Thr Tyr Asn Ile
            420                 425                 430

Ile Leu Met Asp Phe Ala Lys Thr Asn Ser Leu Met Met His Phe Gly
        435                 440                 445
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Cys Phe Arg Thr Tyr Val
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<210> 30
<211> 1386
<212> DNA
<213> Oryza sativa

<400> 30
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ggccgcgcgg ggggcaatgg cgccgaggac gcacgccacg tgttcgacga attgcttcgg 120
cgtggcaagg gcgccacgat ctacggcttg aaccgcgccc tcgacgacgt cgcgcgtcac 180
agccccgcgg ccgccgtgtc ccgctacaac cgcatggccc gagccggcgc cgacgaggta 240
actcccaact tgtacaccta cagcgttctc atcggttgct gctgccgggc gggccgcttg 300
gacctcggtt tcgcggcctt gggcaatgtc attaagaagg gatttagagt ggaagccatc 360
accttcactc ctctgctcaa gggcctctgt gccgacaaga ggacgagcga cgcaatggac 420
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ggcttcttca aagaggggga tccggacaaa gcttacgcta cataccatga aatgtttgac 660
caggggattt tgccagatgt tgtgacttac agctctatta tcgctgcctt atgcaaggct 720
caagctatgg acaaggccat ggaggtactt aacaccatgg ttaagaatgg tgtcatgcct 780
aattgcagga catataatag tattgtgcac ggatattgct cttcagggca gttgacagag 840
gctattggat ttctcaaaat gatgtgcagt gatggtgtcg aaccagatgt tgttacttgt 900
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gaaaaagtag atgaggcgat gcttgtattc agcaaaatga ggcagcaagg attgagtccg 1200
aatgcagtga actacagaac agtcatagat gtactctgca agctaggcag agtatacgat 1260
gcagtgctta ccttaaagca gatgatcaat gaaggactaa cccctgacat cattgtatat 1320
acccccctaa ttcatggttt ttgtacctgt gacaaatggg agaaggctga ggagttaatt 1380
ttttaa 1386

<210> 31
<211> 461
<212> PRT
<213> Oryza sativa

<400> 31
Met Ala Arg Arg Ala Ala Ser Arg Ala Val Gly Ser Glu Gly Ser Ile
1 5 10 15

Gln Gly Arg Gly Gly Arg Ala Gly Gly Asn Gly Ala Glu Asp Ala Arg
20 25 30

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His Val Phe Asp Glu Leu Leu Arg Arg Gly Lys Gly Ala Thr Ile Tyr
         35                  40                  45

Gly Leu Asn Arg Ala Leu Asp Asp Val Ala Arg His Ser Pro Ala Ala
     50                  55                  60

Ala Val Ser Arg Tyr Asn Arg Met Ala Arg Ala Gly Ala Asp Glu Val
 65                  70                  75                  80

Thr Pro Asn Leu Tyr Thr Tyr Ser Val Leu Ile Gly Cys Cys Cys Arg
                 85                  90                  95

Ala Gly Arg Leu Asp Leu Gly Phe Ala Ala Leu Gly Asn Val Ile Lys
            100                 105                 110

Lys Gly Phe Arg Val Glu Ala Ile Thr Phe Thr Pro Leu Leu Lys Gly
        115                 120                 125

Leu Cys Ala Asp Lys Arg Thr Ser Asp Ala Met Asp Ile Val Leu Cys
    130                 135                 140

Arg Met Thr Gln Leu Gly Cys Ile Pro Asn Val Phe Ser Cys Thr Ile
145                 150                 155                 160

Leu Leu Lys Gly Leu Cys Asp Glu Asn Arg Ser Gln Glu Ala Leu Glu
                165                 170                 175

Leu Leu Gln Met Met Pro Asp Asp Gly Gly Asp Cys Pro Pro Asp Val
            180                 185                 190

Val Leu Tyr Asn Thr Val Ile Asn Gly Phe Phe Lys Glu Gly Asp Pro
        195                 200                 205

Asp Lys Ala Tyr Ala Thr Tyr His Glu Met Phe Asp Gln Gly Ile Leu
    210                 215                 220

Pro Asp Val Val Thr Tyr Ser Ser Ile Ile Ala Ala Leu Cys Lys Ala
225                 230                 235                 240

Gln Ala Met Asp Lys Ala Met Glu Val Leu Asn Thr Met Val Lys Asn
                245                 250                 255

Gly Val Met Pro Asn Cys Arg Thr Tyr Asn Ser Ile Val His Gly Tyr
            260                 265                 270

Cys Ser Ser Gly Gln Leu Thr Glu Ala Ile Gly Phe Leu Lys Met Met
        275                 280                 285
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Cys Ser Asp Gly Val Glu Pro Asp Val Val Thr Cys Asn Leu Leu Met
    290                 295                 300

Asp Tyr Leu Cys Lys Asn Arg Arg Cys Thr Glu Ala Arg Lys Ile Phe
305                 310                 315                 320

Asn Ser Met Thr Lys Cys Gly Leu Lys Pro Asp Ile Thr Thr Tyr Cys
                325                 330                 335

Thr Leu Leu Gln Gly Tyr Ala Thr Lys Gly Ala Leu Val Glu Met His
            340                 345                 350

Asp Leu Leu Asp Leu Met Val Trp Asn Gly Ile Gln Pro Asn His His
        355                 360                 365

Val Phe Asn Ile Leu Ile Cys Ala Tyr Ala Lys Gln Glu Lys Val Asp
    370                 375                 380

Glu Ala Met Leu Val Phe Ser Lys Met Arg Gln Gln Gly Leu Ser Pro
385                 390                 395                 400

Asn Ala Val Asn Tyr Arg Thr Val Ile Asp Val Leu Cys Lys Leu Gly
                405                 410                 415

Arg Val Tyr Asp Ala Val Leu Thr Leu Lys Gln Met Ile Asn Glu Gly
            420                 425                 430

Leu Thr Pro Asp Ile Ile Val Tyr Thr Pro Leu Ile His Gly Phe Cys
        435                 440                 445

Thr Cys Asp Lys Trp Glu Lys Ala Glu Glu Leu Ile Phe
    450                 455                 460
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<210> 32
<211> 1521
<212> DNA
<213> Oryza sativa

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ttcgacgaat tgctccggcg aggcatcggc gctccgatcc gcagcttgaa cggcgctctc 180
gccgacgtcg cgcgcgacaa ccccgcggcc gctgtgtccc gcttcaaccg catggcacga 240
gctggtgcca gcatggtaac tcccaccgtg cacacctatg gcatcctcat cggctgctgc 300
tgcagtgcgg gccgcttaga cctcggtttc gcggccttgg gccatgtcgt taagaaggga 360
ttcagagtgg aacccatcat ctttaatcct ctgctcaagg gcctctgtgc agacaagagg 420
acggacgacg caatggacat agtgctccgt ggaatgaccg agctcagctg cgtgccaaat 480

gtcttctccc acaccattat tctcaaggga ctctgtcatg agaacagaag ccaagaagct 540
ctcgagctgc tccacatgat ggctgatgat ggaggaggct gcttacctaa tgttgtgtca 600
tacagcaccg tcatcgatgg cctcttgaaa ggaggggatc cggacaaagc ctacgctaca 660
taccgtgaaa tgcttgaccg gaggattttg ccaaatgttg tgatttacag ctccattatt 720
gctgccctat gcaagggtca agcaatggac aaggccatgg aggtacacga taggatggtt 780
aagaatggag ttacacccaa ttgcttcacg tatactagtc ttgtgcatgg attttgctct 840
tcagggcagt tgacagaggc tattaaattt ctagaaaaga tgtgcagcaa tggtgttgaa 900
ccaaatgttg ttacttatag ctcgtttatg gactatctct gcaagaacgg aagatgcaca 960
gaagctagaa agatttttga ttctatggtc aagaggggcc taaagcctga tattactacc 1020
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tttgatttga tggtacaaag tgatatgcaa cccgatcatt atgtcttcaa cacactaata 1140
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actgcaaaag aattctatgt acagattatc aaaagtggca aaaaagatct tatagaacag 1440
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<210> 33
<211> 506
<212> PRT
<213> Oryza sativa

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1 5 10 15

Pro Arg Ser Glu Gly Thr Ile Gln Asp Arg Ala Arg Val Gly Ser Gly
20 25 30

Gly Ala Glu Asp Ala Leu Asp Val Phe Asp Glu Leu Leu Arg Arg Gly
35 40 45

Ile Gly Ala Pro Ile Arg Ser Leu Asn Gly Ala Leu Ala Asp Val Ala
50 55 60

Arg Asp Asn Pro Ala Ala Ala Val Ser Arg Phe Asn Arg Met Ala Arg
65 70 75 80

Ala Gly Ala Ser Met Val Thr Pro Thr Val His Thr Tyr Gly Ile Leu
85 90 95

Ile Gly Cys Cys Cys Ser Ala Gly Arg Leu Asp Leu Gly Phe Ala Ala
100 105 110

Leu Gly His Val Val Lys Lys Gly Phe Arg Val Glu Pro Ile Ile Phe

```
        115                 120                 125

Asn Pro Leu Leu Lys Gly Leu Cys Ala Asp Lys Arg Thr Asp Asp Ala
    130                 135                 140

Met Asp Ile Val Leu Arg Gly Met Thr Glu Leu Ser Cys Val Pro Asn
145                 150                 155                 160

Val Phe Ser His Thr Ile Ile Leu Lys Gly Leu Cys His Glu Asn Arg
                165                 170                 175

Ser Gln Glu Ala Leu Glu Leu Leu His Met Met Ala Asp Asp Gly Gly
            180                 185                 190

Gly Cys Leu Pro Asn Val Val Ser Tyr Ser Thr Val Ile Asp Gly Leu
        195                 200                 205

Leu Lys Gly Gly Asp Pro Asp Lys Ala Tyr Ala Thr Tyr Arg Glu Met
    210                 215                 220

Leu Asp Arg Arg Ile Leu Pro Asn Val Val Ile Tyr Ser Ser Ile Ile
225                 230                 235                 240

Ala Ala Leu Cys Lys Gly Gln Ala Met Asp Lys Ala Met Glu Val His
                245                 250                 255

Asp Arg Met Val Lys Asn Gly Val Thr Pro Asn Cys Phe Thr Tyr Thr
            260                 265                 270

Ser Leu Val His Gly Phe Cys Ser Ser Gly Gln Leu Thr Glu Ala Ile
        275                 280                 285

Lys Phe Leu Glu Lys Met Cys Ser Asn Gly Val Glu Pro Asn Val Val
    290                 295                 300

Thr Tyr Ser Ser Phe Met Asp Tyr Leu Cys Lys Asn Gly Arg Cys Thr
305                 310                 315                 320

Glu Ala Arg Lys Ile Phe Asp Ser Met Val Lys Arg Gly Leu Lys Pro
                325                 330                 335

Asp Ile Thr Thr Tyr Ser Ser Leu Leu His Gly Tyr Ala Ile Glu Gly
            340                 345                 350

Ala Leu Val Glu Met His Gly Leu Phe Asp Leu Met Val Gln Ser Asp
        355                 360                 365

Met Gln Pro Asp His Tyr Val Phe Asn Thr Leu Ile Tyr Ala Ser Ala
```

370 375 380

Lys Gln Gly Lys Val Asp Glu Ala Met Leu Val Phe Ser Lys Met Arg
385 390 395 400

Gln Gln Gly Leu Lys Pro Asn Cys Val Thr Tyr Ser Thr Leu Ile Asn
405 410 415

Gly Tyr Cys Lys Ile Thr Arg Met Glu Asn Ala Leu Ala Leu Phe Gln
420 425 430

Glu Met Val Ser Asn Gly Val Ser Pro Asn Phe Ile Thr Tyr Asn Ile
435 440 445

Met Leu Gln Gly Leu Phe Arg Thr Gly Arg Thr Ala Thr Ala Lys Glu
450 455 460

Phe Tyr Val Gln Ile Ile Lys Ser Gly Lys Lys Asp Leu Ile Glu Gln
465 470 475 480

Gly Leu Leu Glu Glu Leu Asp Asp Leu Phe Leu Ser Met Glu Asp Asn
485 490 495

Asp Cys Ser Thr Val Ser Thr Pro Ala Cys
500 505

<210> 34
<211> 1884
<212> DNA
<213> Oryza sativa

<400> 34
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gggcgagggg gccgcgcggg gggcagtggc ggtggcgcgg aggacgcacg ccacgtgttc 120
gacgaattgc tccgtcgtgg cataccagat gtcttctcct acaatattct tctcaacggg 180
ctgtgtgatg agaacagaag ccaagaagct ctcgagttac tgcacataat ggctgatgat 240
ggaggtgact gcccacctga tgtggtgtcg tacagcaccg tcatcaatgg cttcttcaag 300
gaggggatc tggacaaaat gcttgaccag aggatttcgc caaatgttgt gacctacaac 360
tctattattg ctgcgctatg caaggctcaa actgtggaca aggccatgga ggtacttacc 420
accatggtta agagtggtgt catgcctgat tgcatgacat ataatagtat tgtgcatggg 480
ttttgctctt cagggcagcc gaaagaggct attgtatttc tcaaaaagat gcgcagtgat 540
ggtgtcgaac cagatgttgt tacttataac tcgctcatgg attatctttg caagaacgga 600
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catggtctct tggatttgat ggtacgaaac ggtatccacc ctaatcatta tgttttcagc 780
attctagtat gtgcatacgc taaacaagag aaagtagaag aggcaatgct tgtattcagc 840
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ctttgcaagt caggtagagt agaagatgct atgctttatt ttgagcagat gatcgatgaa 960
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aatttcattg ttagggaact gttgcagaga ggtgagataa ccagggctgg cacttacctt 1740
tccatgattg atgagaagca cttttccctc gaagcatcca ctgcttcctt gtttatagat 1800
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tttatagaat ctttgagctg ctga 1884

<210> 35
<211> 627
<212> PRT
<213> Oryza sativa

<400> 35
Met Ala Arg Arg Ala Ala Ser Arg Ala Ala Gly Ala Leu Arg Ser Glu
1 5 10 15

Gly Ser Ile Gln Gly Arg Gly Gly Arg Ala Gly Gly Ser Gly Gly Gly
20 25 30

Ala Glu Asp Ala Arg His Val Phe Asp Glu Leu Leu Arg Arg Gly Ile
35 40 45

Pro Asp Val Phe Ser Tyr Asn Ile Leu Leu Asn Gly Leu Cys Asp Glu
50 55 60

Asn Arg Ser Gln Glu Ala Leu Glu Leu Leu His Ile Met Ala Asp Asp
65 70 75 80

Gly Gly Asp Cys Pro Pro Asp Val Val Ser Tyr Ser Thr Val Ile Asn
85 90 95

Gly Phe Phe Lys Glu Gly Asp Leu Asp Lys Met Leu Asp Gln Arg Ile
100 105 110

Ser Pro Asn Val Val Thr Tyr Asn Ser Ile Ile Ala Ala Leu Cys Lys
115 120 125

```
Ala Gln Thr Val Asp Lys Ala Met Glu Val Leu Thr Thr Met Val Lys
    130                 135                 140

Ser Gly Val Met Pro Asp Cys Met Thr Tyr Asn Ser Ile Val His Gly
145                 150                 155                 160

Phe Cys Ser Ser Gly Gln Pro Lys Glu Ala Ile Val Phe Leu Lys Lys
                165                 170                 175

Met Arg Ser Asp Gly Val Glu Pro Asp Val Val Thr Tyr Asn Ser Leu
            180                 185                 190

Met Asp Tyr Leu Cys Lys Asn Gly Arg Cys Thr Glu Ala Arg Lys Ile
        195                 200                 205

Phe Asp Ser Met Thr Lys Arg Gly Leu Lys Pro Asp Ile Thr Thr Tyr
    210                 215                 220

Gly Thr Leu Leu Gln Gly Tyr Ala Thr Lys Gly Ala Leu Val Glu Met
225                 230                 235                 240

His Gly Leu Leu Asp Leu Met Val Arg Asn Gly Ile His Pro Asn His
                245                 250                 255

Tyr Val Phe Ser Ile Leu Val Cys Ala Tyr Ala Lys Gln Glu Lys Val
            260                 265                 270

Glu Glu Ala Met Leu Val Phe Ser Lys Met Arg Gln Gln Gly Leu Asn
        275                 280                 285

Pro Asn Ala Val Thr Tyr Gly Thr Val Ile Asp Val Leu Cys Lys Ser
    290                 295                 300

Gly Arg Val Glu Asp Ala Met Leu Tyr Phe Glu Gln Met Ile Asp Glu
305                 310                 315                 320

Gly Leu Arg Pro Asp Ser Ile Val Tyr Asn Ser Leu Ile His Ser Leu
                325                 330                 335

Cys Ile Phe Asp Lys Trp Glu Lys Ala Glu Glu Leu Phe Leu Glu Met
            340                 345                 350

Leu Asp Arg Gly Ile Cys Leu Ser Thr Ile Phe Phe Asn Ser Ile Ile
        355                 360                 365

Asp Ser His Cys Lys Glu Gly Arg Val Ile Glu Ser Gly Lys Leu Phe
    370                 375                 380
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Asp Leu Met Val Arg Ile Gly Val Lys Pro Asp Ile Ile Thr Leu Gly
385                 390                 395                 400

Arg Phe Leu Gly Ser Ala Arg Arg Asp Tyr Ser Leu Phe Val Asn Ile
                405                 410                 415

Tyr Phe Ile Phe Thr Asn Met Ser Asn Thr Gly Asp Lys Glu Lys Glu
            420                 425                 430

Thr Pro Val Asn Thr Asn Gly Gly Asn Thr Ala Ser Asn Ser Ser Gly
        435                 440                 445

Gly Pro Phe Leu Gly Thr Tyr Asn Ile Ile Leu His Gly Leu Cys Lys
    450                 455                 460

Asn Lys Leu Thr Asp Asp Ala Leu Arg Met Phe Gln Asn Leu Cys Leu
465                 470                 475                 480

Met Asp Leu Lys Leu Glu Ala Arg Thr Phe Asn Ile Met Ile Asp Ala
                485                 490                 495

Leu Leu Lys Val Gly Arg Asn Asp Glu Ala Lys Asp Leu Phe Val Ala
            500                 505                 510

Phe Ser Ser Asn Gly Leu Val Pro Asn Tyr Trp Thr Tyr Arg Leu Met
        515                 520                 525

Ala Glu Asn Ile Ile Gly Gln Gly Leu Leu Glu Glu Leu Asp Gln Leu
    530                 535                 540

Phe Leu Ser Met Glu Asp Asn Gly Cys Thr Val Asp Ser Gly Met Leu
545                 550                 555                 560

Asn Phe Ile Val Arg Glu Leu Leu Gln Arg Gly Glu Ile Thr Arg Ala
                565                 570                 575

Gly Thr Tyr Leu Ser Met Ile Asp Glu Lys His Phe Ser Leu Glu Ala
            580                 585                 590

Ser Thr Ala Ser Leu Phe Ile Asp Leu Leu Ser Gly Gly Lys Tyr Gln
        595                 600                 605

Glu Tyr His Ile Phe Leu Pro Glu Lys Tyr Lys Ser Phe Ile Glu Ser
    610                 615                 620

Leu Ser Cys
625
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<210> 36
<211> 1554
<212> DNA
<213> Oryza sativa

<400> 36
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gctccggtgg ctgggaggtg gcgacgtcgg cggccgaatg tgttcccgag cgccgcgctg 120
gagagccccg agctgcgacg gcatcacgcc gactaccggc cgtgggcggc gcacatggag 180
gcaaagccgg tctacttcgc gtcgaggcgt gcctccgggc ggcccgagct gcagcagcag 240
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tgccaggtcg gtgaccctcc gccgccggcg gcggcggcgg cggcggcagg catggcgcgc 420
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cagggtggta cgacccaaga cctagggcgc gcgggggggca gtggcaccga gggcgcacgc 540
cacgtgctcg acgaattgcc gctacggggc tggggcgcct cgatctacag cttcaaccgc 600
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gcccgagccg gcgccgacga ggtaactccc gacttgtgca cctacagcat tctcatcggt 720
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aagggattta gagtggaagc catcaccttc gctcctctgc tcaagggcct ctgtgccgac 840
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accatggtta agaatggtgt catgcctgat tgcatgacat ataatagtat tctgcatgga 1260
tattgctctt cagggcagcc aaaagaggct attggaacac tcaaaaagat gcgcagtgat 1320
ggcgtcgaac caaatgttgt tacttataga tcactgatga attatctttg caagaatgga 1380
agatgcaccg aagctagaaa gattttcgat tctatgacca agaggggcct agagcctgat 1440
attgctacct atcgtaccct gcttcagggg tatgctacca aaggagccct tgttgagatg 1500
catgctctct tggatttgat ggatcctgag ttctacaagt atttggagaa gtga 1554

<210> 37
<211> 517
<212> PRT
<213> Oryza sativa

<400> 37
Met Ala Arg Arg Gly Arg Arg Tyr Cys Arg Ala Glu Gly Thr Glu Glu
1 5 10 15

Arg Gly Thr Gly Ala Pro Val Ala Gly Arg Trp Arg Arg Arg Arg Pro
20 25 30

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Asn Val Phe Pro Ser Ala Ala Leu Glu Ser Pro Glu Leu Arg Arg His
         35                  40                  45

His Ala Asp Tyr Arg Pro Trp Ala Ala His Met Glu Ala Lys Pro Val
     50                  55                  60

Tyr Phe Ala Ser Arg Arg Ala Ser Gly Arg Pro Glu Leu Gln Gln Gln
 65                  70                  75                  80

Leu Val Arg Pro Thr Pro Ile Trp Ala Asp Trp Ala Asp Leu Ser Leu
                 85                  90                  95

Pro Glu Arg Arg Pro Ile Trp Ala Val His Pro Arg Arg Pro Ala Asn
            100                 105                 110

Arg Thr Val Gly Val Leu Leu Tyr Cys Gln Val Gly Asp Pro Pro Pro
        115                 120                 125

Pro Ala Ala Ala Ala Ala Ala Ala Gly Met Ala Arg Arg Val Thr Thr
    130                 135                 140

Leu Thr Arg Ala Arg Thr Arg Ala Arg Gly Gly Gly Val Pro Ser Ala
145                 150                 155                 160

Gln Gly Gly Thr Thr Gln Asp Leu Gly Arg Ala Gly Gly Ser Gly Thr
                165                 170                 175

Glu Gly Ala Arg His Val Leu Asp Glu Leu Pro Leu Arg Gly Trp Gly
            180                 185                 190

Ala Ser Ile Tyr Ser Phe Asn Arg Thr Leu Thr Asp Val Ala Arg Asp
        195                 200                 205

Ser Pro Ala Ala Ala Val Ser Leu Phe Asn Arg Met Ala Arg Ala Gly
    210                 215                 220

Ala Asp Glu Val Thr Pro Asp Leu Cys Thr Tyr Ser Ile Leu Ile Gly
225                 230                 235                 240

Cys Cys Cys Arg Ala Gly Arg Leu Asp Leu Gly Phe Ala Ala Leu Gly
                245                 250                 255

Asn Val Ile Lys Lys Gly Phe Arg Val Glu Ala Ile Thr Phe Ala Pro
            260                 265                 270

Leu Leu Lys Gly Leu Cys Ala Asp Lys Arg Thr Ser Asp Ala Met Asp
        275                 280                 285
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Ile Val Leu Arg Arg Met Thr Glu Leu Ser Cys Met Pro Asp Val Phe
    290                 295                 300

Ser Cys Thr Ile Leu Leu Lys Gly Leu Cys Asp Glu Asn Arg Ser Gln
305                 310                 315                 320

Glu Ala Leu Glu Leu Leu His Met Met Ala Asp Asp Arg Gly Gly Gly
                325                 330                 335

Ser Pro Pro Asp Val Val Ser Tyr Thr Thr Val Ile Asn Gly Phe Phe
            340                 345                 350

Lys Glu Gly Asp Ser Asp Lys Ala Tyr Ser Thr Tyr His Glu Met Leu
        355                 360                 365

Asp Arg Arg Ile Ser Pro Asn Val Val Thr Tyr Ser Ser Ile Ile Ala
    370                 375                 380

Ala Leu Cys Lys Ala Gln Ala Met Asp Lys Ala Met Glu Val Leu Asn
385                 390                 395                 400

Thr Met Val Lys Asn Gly Val Met Pro Asp Cys Met Thr Tyr Asn Ser
                405                 410                 415

Ile Leu His Gly Tyr Cys Ser Ser Gly Gln Pro Lys Glu Ala Ile Gly
            420                 425                 430

Thr Leu Lys Lys Met Arg Ser Asp Gly Val Glu Pro Asn Val Val Thr
        435                 440                 445

Tyr Arg Ser Leu Met Asn Tyr Leu Cys Lys Asn Gly Arg Cys Thr Glu
    450                 455                 460

Ala Arg Lys Ile Phe Asp Ser Met Thr Lys Arg Gly Leu Glu Pro Asp
465                 470                 475                 480

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Arg Tyr Thr Phe Ser Thr Leu Ile His Gly Leu Cys Lys Val Gly Ser
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Tyr Cys Lys Ile Gly Asp Leu Gln Leu Ala Glu Ser Tyr Phe Arg Ala
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Phe Asp Glu Met Val Ala Lys Arg Ile Lys Ala Asn Ala Val Thr Tyr
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Gln Met Ala Phe His Ile His Asp Ile Met Leu Cys Arg Gly Leu Val
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Gly Ile Lys Leu Arg Lys Phe Ala Tyr Thr Thr Leu Ile Lys Ala Gln

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Cys Ala Lys Gly Met Pro Ile Asn Ala Val Leu Leu Val Gly Lys Leu
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Leu Asp Ala Gly Phe Glu Ala Ser Ile Glu Asp Phe Ser Ala Ala Ile
740 745 750

Asn Arg Leu Cys Lys Arg Gln Phe Ala Lys Glu Ala Phe Met Phe Val
755 760 765

Pro Ile Met Leu Ser Val Gly Ile Tyr Pro Asp Thr Gln Ile Tyr Cys
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Arg Leu Arg Ser Gly Ile Val Asp Ile Lys Lys Asp Asp Ala Ile Ala
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Thr Cys Phe Ala Tyr Ser Val Leu Gly Lys Val Met Lys Leu Gly Tyr
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ggaaatgtga ttatcccatt caaagatact tgacagatgt ctcatgatgc ttatttgact 4380
cagaagaata ttcagaaaag gcatgtagat gtgcagcaaa tgacagagta tgtgcaatgg 4440
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tagtttattt gagaaagtta tatatataca atgtatgaac tgatattctt tgataatgat 6660
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<210> 43
<211> 591
<212> PRT
<213> Petunia sp.

<400> 43

Met Met Arg Ile Ser Val Arg Tyr Cys Leu Asn Gly Asn Pro Phe Phe
1 5 10 15

Ser Phe Phe Ala Tyr Ser Ile Ala Pro Arg His Tyr Ser Thr Asn Thr
20 25 30

Cys Ser Ile Ser Val Lys Gly Asn Phe Gly Val Ser Asn Glu Phe Gln
35 40 45

Asn Val Lys Cys Leu Asp Asp Ala Phe Ser Leu Phe Arg Gln Met Val
50 55 60

Arg Thr Lys Pro Leu Pro Ser Val Ala Ser Phe Ser Lys Leu Leu Lys
65 70 75 80

Ala Met Val His Met Lys His Tyr Ser Ser Val Val Ser Leu Phe Arg
85 90 95

Glu Ile His Lys Leu Arg Ile Pro Val His Glu Phe Ile Leu Ser Ile
100 105 110

Val Val Asn Ser Cys Cys Leu Met His Arg Thr Asp Leu Gly Phe Ser
115 120 125

Val Leu Ala Ile His Phe Lys Lys Gly Ile Pro Tyr Asn Glu Val Thr
130 135 140

Phe Thr Thr Leu Ile Arg Gly Leu Phe Ala Glu Asn Lys Val Lys Asp
145 150 155 160

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Ala Val His Leu Phe Lys Lys Leu Val Arg Glu Asn Ile Cys Glu Pro
                165                 170                 175

Asn Glu Val Met Tyr Gly Thr Val Met Asn Gly Leu Cys Lys Lys Gly
            180                 185                 190

His Thr Gln Lys Ala Phe Asp Leu Leu Arg Leu Met Glu Gln Gly Ser
        195                 200                 205

Thr Lys Pro Asn Thr Arg Thr Tyr Thr Ile Val Ile Asp Ala Phe Cys
    210                 215                 220

Lys Asp Gly Met Leu Asp Gly Ala Thr Ser Leu Leu Asn Glu Met Lys
225                 230                 235                 240

Gln Lys Ser Ile Pro Pro Asp Ile Phe Thr Tyr Ser Thr Leu Ile Asp
                245                 250                 255

Ala Leu Cys Lys Leu Ser Gln Trp Glu Asn Val Arg Thr Leu Phe Leu
            260                 265                 270

Glu Met Ile His Leu Asn Ile Tyr Pro Asn Val Cys Thr Phe Asn Ser
        275                 280                 285

Val Ile Asp Gly Leu Cys Lys Glu Gly Lys Val Glu Asp Ala Glu Glu
    290                 295                 300

Ile Met Arg Tyr Met Ile Glu Lys Gly Val Asp Pro Asp Val Ile Thr
305                 310                 315                 320

Tyr Asn Met Ile Ile Asp Gly Tyr Gly Leu Arg Gly Gln Val Asp Arg
                325                 330                 335

Ala Arg Glu Ile Phe Asp Ser Met Ile Asn Lys Ser Ile Glu Pro Asp
            340                 345                 350

Ile Ile Ser Tyr Asn Ile Leu Ile Asn Gly Tyr Ala Arg Gln Lys Lys
        355                 360                 365

Ile Asp Glu Ala Met Gln Val Cys Arg Glu Ile Ser Gln Lys Gly Leu
    370                 375                 380

Lys Pro Ser Ile Val Thr Cys Asn Val Leu Leu His Gly Leu Phe Glu
385                 390                 395                 400

Leu Gly Arg Thr Lys Ser Ala Gln Asn Phe Phe Asp Glu Met Leu Ser
                405                 410                 415
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Ala Gly His Ile Pro Asp Leu Tyr Thr His Cys Thr Leu Leu Gly Gly
420 425 430

Tyr Phe Lys Asn Gly Leu Val Glu Glu Ala Met Ser His Phe His Lys
435 440 445

Leu Glu Arg Arg Arg Glu Asp Thr Asn Ile Gln Ile Tyr Thr Ala Val
450 455 460

Ile Asp Gly Leu Cys Lys Asn Gly Lys Leu Asp Lys Ala His Ala Thr
465 470 475 480

Phe Glu Lys Leu Pro Leu Ile Gly Leu His Pro Asp Val Ile Thr Tyr
485 490 495

Thr Ala Met Ile Ser Gly Tyr Cys Gln Glu Gly Leu Leu Asp Glu Ala
500 505 510

Lys Asp Met Leu Arg Lys Met Glu Asp Asn Gly Cys Leu Ala Asp Asn
515 520 525

Arg Thr Tyr Asn Val Ile Val Arg Gly Phe Leu Arg Ser Asn Lys Val
530 535 540

Ser Glu Met Lys Ala Phe Leu Glu Glu Ile Ala Gly Lys Ser Phe Ser
545 550 555 560

Phe Glu Ala Ala Thr Val Glu Leu Leu Met Asp Ile Ile Ala Glu Asp
565 570 575

Pro Ser Ile Thr Arg Lys Met His Trp Ile Lys Leu His Ile Ala
580 585 590

<210> 44
<211> 1779
<212> DNA
<213> Petunia sp.

<400> 44
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tttggggttt ctaatgaatt tgagaatgtt aagtgtttag atgatgcttt cagtttgttc 180
cgtcaaatgg ttagaactaa gcctcttcct tctgttgtct ctttctctaa attgttgaaa 240
gctttggtac atatgaagca ttactcttct gttgtttctc tttttcgaga aatccacaaa 300
ttacgtattc ctgttcatga attcatcttg agcattgtgg ttaacagttg ttgccttatg 360
catcgtaccg atctcggatt ttctgtatta gccattcact tcaagaaagg tattccattt 420
aatcaagtta tctttaacac cttactaagg ggactctttg ctgaaaataa ggttaaagat 480

gctgttcatt tgttcaaaaa gttggtgagg gagaatatat gtgagcctaa tgaagtcatg 540
tatggaacgg tcatgaatgg gctttgcaaa aagggccata ctcaaaaagc ttttgatttg 600
ctccggttaa tggaacaagg aagtactaag cccaatacat gtatctatag cattgttatc 660
gatgcctttt gcaaagatgg gatgctagat ggtgctacca gccttttgaa tgagatgaaa 720
caaaaaagca ttcctcccga cattttact tatagcactt taattgatgc tttgtgtaag 780
ttaagtcagt gggaaaatgt taggactttg ttccttgaga tgatacatct taatatttat 840
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gacgctgagg aaataatgag atacatgatt gaaaaaggtg tagaccctga tgtgatcacc 960
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aatggatatg ccaggcaaaa gaaaatagac gaggcaatgc aagtctgccg tgaaatttct 1140
caaaagggat tgaaacctag tattgttacc tgcaatgttc tcttgcatgg tctttttgaa 1200
cttggaagaa ctaaatctgc acaaaatttc tttgatgaga tgctatctgc ggggcacata 1260
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agtggatatt gtcaagaagg gttgttagat gaagctaaag atatgctaag gaaaatggag 1560
gacaatggtt gtttggcaga caaccgaaca tacaatgtta ttgtgcgggg atttctcaga 1620
agcaataaag ttagtgaaat gaaggctttt ctggaggaaa tagctgggaa gagcttctca 1680
tttgaggcag ctactgtaga gttattgatg gatattatag cagaggatcc ttctttgctt 1740
aacatgattc cagaatttca ccgggataat aagaagtga 1779

<210> 45
<211> 592
<212> PRT
<213> Petunia sp.

<400> 45
Met Met Arg Ile Ala Val Arg Tyr Cys Leu Asn Gly Asn Pro Phe Phe
1 5 10 15

Ser Phe Phe Ala Tyr Ser Ile Ala Pro Arg His Tyr Ser Thr Asn Thr
20 25 30

Arg Ser Ile Ser Val Lys Gly Asn Phe Gly Val Ser Asn Glu Phe Glu
35 40 45

Asn Val Lys Cys Leu Asp Asp Ala Phe Ser Leu Phe Arg Gln Met Val
50 55 60

Arg Thr Lys Pro Leu Pro Ser Val Val Ser Phe Ser Lys Leu Leu Lys
65 70 75 80

Ala Leu Val His Met Lys His Tyr Ser Ser Val Val Ser Leu Phe Arg
85 90 95

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Glu Ile His Lys Leu Arg Ile Pro Val His Glu Phe Ile Leu Ser Ile
            100                 105                 110

Val Val Asn Ser Cys Cys Leu Met His Arg Thr Asp Leu Gly Phe Ser
        115                 120                 125

Val Leu Ala Ile His Phe Lys Lys Gly Ile Pro Phe Asn Gln Val Ile
    130                 135                 140

Phe Asn Thr Leu Leu Arg Gly Leu Phe Ala Glu Asn Lys Val Lys Asp
145                 150                 155                 160

Ala Val His Leu Phe Lys Lys Leu Val Arg Glu Asn Ile Cys Glu Pro
                165                 170                 175

Asn Glu Val Met Tyr Gly Thr Val Met Asn Gly Leu Cys Lys Lys Gly
            180                 185                 190

His Thr Gln Lys Ala Phe Asp Leu Leu Arg Leu Met Glu Gln Gly Ser
        195                 200                 205

Thr Lys Pro Asn Thr Cys Ile Tyr Ser Ile Val Ile Asp Ala Phe Cys
    210                 215                 220

Lys Asp Gly Met Leu Asp Gly Ala Thr Ser Leu Leu Asn Glu Met Lys
225                 230                 235                 240

Gln Lys Ser Ile Pro Pro Asp Ile Phe Thr Tyr Ser Thr Leu Ile Asp
                245                 250                 255

Ala Leu Cys Lys Leu Ser Gln Trp Glu Asn Val Arg Thr Leu Phe Leu
            260                 265                 270

Glu Met Ile His Leu Asn Ile Tyr Pro Asn Val Cys Thr Phe Asn Ser
        275                 280                 285

Val Ile Asp Gly Leu Cys Lys Glu Gly Lys Val Glu Asp Ala Glu Glu
    290                 295                 300

Ile Met Arg Tyr Met Ile Glu Lys Gly Val Asp Pro Asp Val Ile Thr
305                 310                 315                 320

Tyr Asn Met Ile Ile Asp Gly Tyr Gly Leu Arg Gly Gln Val Asp Arg
                325                 330                 335

Ala Arg Glu Ile Phe Asp Ser Met Ile Asn Lys Ser Ile Glu Pro Asn
            340                 345                 350
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Ile Ile Ser Tyr Asn Ile Leu Ile Asn Gly Tyr Ala Arg Gln Lys Lys
355 360 365

Ile Asp Glu Ala Met Gln Val Cys Arg Glu Ile Ser Gln Lys Gly Leu
370 375 380

Lys Pro Ser Ile Val Thr Cys Asn Val Leu Leu His Gly Leu Phe Glu
385 390 395 400

Leu Gly Arg Thr Lys Ser Ala Gln Asn Phe Phe Asp Glu Met Leu Ser
405 410 415

Ala Gly His Ile Pro Asp Leu Tyr Thr His Cys Thr Leu Leu Gly Gly
420 425 430

Tyr Phe Lys Asn Gly Leu Val Glu Glu Ala Met Ser His Phe His Lys
435 440 445

Leu Glu Arg Arg Arg Glu Asp Thr Asn Ile Gln Ile Tyr Thr Ala Val
450 455 460

Ile Asp Gly Leu Cys Lys Asn Gly Lys Leu Asp Lys Ala His Ala Thr
465 470 475 480

Phe Glu Lys Leu Pro Leu Ile Gly Leu His Pro Asp Val Ile Thr Tyr
485 490 495

Thr Ala Met Ile Ser Gly Tyr Cys Gln Glu Gly Leu Leu Asp Glu Ala
500 505 510

Lys Asp Met Leu Arg Lys Met Glu Asp Asn Gly Cys Leu Ala Asp Asn
515 520 525

Arg Thr Tyr Asn Val Ile Val Arg Gly Phe Leu Arg Ser Asn Lys Val
530 535 540

Ser Glu Met Lys Ala Phe Leu Glu Glu Ile Ala Gly Lys Ser Phe Ser
545 550 555 560

Phe Glu Ala Ala Thr Val Glu Leu Leu Met Asp Ile Ile Ala Glu Asp
565 570 575

Pro Ser Leu Leu Asn Met Ile Pro Glu Phe His Arg Asp Asn Lys Lys
580 585 590

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
tgcacagtgt tatatttaca taccc 25

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
tttatgatac atggatttca acgac 25

<210> 48
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
tgaaaatgac aatcgtaaca gaaaa 25

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
aacattcctc cagacattat taca 24

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
gacgctgagg aaataatgag atac 24

<210> 51
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51
tctagaaaaa atgaaggggg aatcaat 27

<210> 52
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 52
gaattcactt tgctctcacg ataaactaag a 31